

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 23, 1999, 12:07:33 ; Search time 70.49 Seconds
(without alignments)
92.283 Million cell updates/sec

Title: US-09-031-087-1
Perfect score: 26
Sequence: 1 gcgttagatgagtcgtgcagcct 26

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	9185	1 Q05956	Sense strand of th
2	26	100.0	9185	1 Q10566	Hepatitis C virus
3	26	100.0	504	1 Q12239	Clone 164/137 enco
4	26	100.0	2116	1 Q12242	Encodes PT-NANBH v
5	26	100.0	202	1 Q14083	HCV-T (1-202). New
6	26	100.0	202	1 Q14084	HCV-T (1-202). New
7	26	100.0	1863	1 Q15363	Fragment of NANBH h
8	26	100.0	1863	1 Q15362	Fragment of NANBH h
9	26	100.0	9416	1 Q21829	Non-A, non-B viral
10	26	100.0	9416	1 Q20268	Non-A, non-B viral
11	26	100.0	807	1 Q20940	PCR-generated frag
12	26	100.0	9400	1 Q21744	Compiled HCV cDNA.
13	26	100.0	9416	1 Q21871	NANBH Hutch c59 is
14	26	100.0	1880	1 Q24467	NANBH hepatitis vir
15	26	100.0	1880	1 Q24466	NANBH hepatitis vir
16	26	100.0	2540	1 Q29628	Hepatitis C virus
17	26	100.0	2540	1 Q29627	Hepatitis C virus
18	26	100.0	483	1 Q32444	HCV core-envelope
19	26	100.0	483	1 Q32445	HCV core-envelope
20	26	100.0	483	1 Q32446	HCV core-envelope
21	26	100.0	483	1 Q32447	HCV core-envelope
22	26	100.0	1554	1 Q32451	HCV core-envelope
23	26	100.0	483	1 Q32453	HCV core-envelope
24	26	100.0	7911	1 Q32436	HCV antigen clone
25	26	100.0	9379	1 Q36209	Composite cDNA for
26	26	100.0	9472	1 Q33282	Korean hepatitis C
27	26	100.0	9391	1 Q38959	Hepatitis C virus
28	26	100.0	194	1 Q43072	-255 to -62 region
29	26	100.0	159	1 Q43069	-255 to -62 region
30	26	100.0	159	1 Q43071	-255 to -62 region
31	26	100.0	194	1 Q43075	-255 to -62 region
32	26	100.0	194	1 Q43073	-255 to -62 region
33	26	100.0	2540	1 Q43889	NANBH hepatitis vir
34	26	100.0	2540	1 Q43888	NANBH hepatitis vir
35	26	100.0	341	1 Q62945	5' untranslated re
36	26	100.0	686	1 Q44921	Hepatitis C virus
37	26	100.0	2033	1 Q64913	Hepatitis C virus
38	26	100.0	4987	1 Q65322	vaccinia virus pro
39	26	100.0	9436	1 Q63499	Blood transmiscibl
40	26	100.0	2540	1 Q63752	NANBH genomic fra
41	26	100.0	2540	1 Q63753	NANBH genomic fra
42	26	100.0	9391	1 Q64175	NANBH E1/E2 gene
43	26	100.0	3461	1 Q64068	Non-A, non-B hepat

ALIGNMENTS

```
RESULT 1
Q05956
ID Q05956 standard; DNA: 9185 BP.
AC Q05956;
DE 23-JAN-1991 (first entry)
DT Sense strand of the compiled Hepatitis C virus cDNA sequence.
KW Hepatitis C virus (HCV); antiviral agent; ss.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT cds 320..9185
FT misc_rna 1..1667
FT /*tag= a
FT /*tag= b
FT /*tag="epitope within this region is claimed"
FT misc_rna 8978..9185
FT /*tag= c
FT /*tag="encodes an epitope that is claimed"
PN EP-388232-A.
PD 19-SEP-1990. 302866.
PF 16-MAR-1990; US-325338.
PR 17-MAR-1989; US-341334.
PR 20-APR-1989; US-341334.
PR 18-MAY-1989; US-355002.
PA (CHIR-) CHIRON CORP.
PI Houghton M, Choo QL, Kuo G;
DR WPI; 90-284418/38.
DR P-PSDB; R08124.
PT Hepatitis C virus DNA - used for producing probes.
PT polypeptides(s), antibodies and anti-sense polynucleotide(s) for
PT diagnosis and therapy.
PS Disclosure; Fig 17; 83pp; English.
CC HCV cDNA libraries were constructed using pooled serum from a
CC chimpanzee with chronic HCV infection. A lambda gt10 library was
CC screened with probes derived from previously isolated clones. The
CC ORF is derived from the overlapping clones b114a, ag30a, CA205a,
CC CA290a, CA216a, p14a, CA167b, CA156e, CA84a, CA59a, K9-1, 26j, 13i,
CC 12f, 14i, 11b, 7f, 8h, 33c, 40b, 37b, 33, 36, 81, 32, 33b, 25c,
CC 14c, 8f, 33f, 39c, 35f, 19g, 26g, 15e, b5a and 16jh. These
CC clones extend the sequence of the HCV genome reported in EP-318216.
CC The upstream region from nucleotides -319 to +1348 (=1-1667 in this
CC file) is covered by clones b114a, 18g, ag30a, CA205a, CA290a,
CC CA216a, p14a, CA167b, CA156e, CA84a and CA59a; nucleotides
CC 8639-8866 (-8978-9185 in this file) are covered by clones b5a and
CC 16jh.
CC See also Q05955.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;
```

Query Match 100.0%; Score 26; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 gcgttagatgagtcgtgcagcct 26
    |||
Db 66 GCGTTAGTAGTGTGCTGCAGCCT 91
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RESULT 2
Q10566
ID Q10566 standard; DNA: 9185 BP.
AC Q10566;
DE 29-APR-1991 (first entry)
DT Hepatitis C virus strain 1 DNA.
KW Hepatitis C virus; HCV-1; non-A, non-B hepatitis; HCV antigen;
KW viral infections; ss.
OS Hepatitis C virus.
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PN EP-414475-A.
PD 27-FEB-1991.
PR 21-AUG-1990; 309120.
PR 25-AUG-1989; US-398667.
PA (CHLR-) CHIRON CORP.
PI Weiner AJ, Steimer KS;
DR WPI; 91-059670/09.
PT Cell lines infected with hepatitis C virus - are used as source
PT of antigens for detection of HCV antibodies, for vaccines, and
PT for screening anti-viral agents
PS Disclosure; fig 1; 24pp; English.
CC This is a hepatitis C virus (HCV) composite cDNA sequence, deduced
CC using overlapping clones, a compsn. contg. the antigenic protein
CC encoded by this sequence is useful for detecting anti-HCV anti-
CC bodies (Abs) and for screening an agent which inhibits HCV replic-
CC ation. A cell line infected with this virus can be used as a
CC source of antigens. The antigen is useful for preparing vaccines
CC for treating viral infections. See also Q10567.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;

Query Match 100.0%; Score 26; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgtagtagtgagtgctgcgcgcct 26
    |||||
Db 66 GCGTTAGTAGTGAGTGCTGCAGCCT 91

RESULT 3
Q12239
ID Q12239 standard; DNA; 504 BP.
AC Q12239;
DT 06-SEP-1991 (first entry)
DE Clone 164/137 encoding PT-NANBH virus antigenic portion.
KW Post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 308..504
FT /*tag= a
FT /product= start of PT-NANBH polyprotein
PN GB2239245-A.
PD 26-JUN-1991.
PR 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI; 91-187584/26.
DR P-PSDB; R12597.
PT Post-transfusional non-A non-B hepatitis poly-peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 71-72; 108pp; English.
CC This sequence probably encodes viral structural proteins of the
CC PT-NANBH viral genome having antigenic properties. It was
CC isolated from serum of humans infected by the virus.
CC See also Q12236-8 and Q12240-Q12242.
SQ Sequence 504 BP; 106 A; 147 C; 153 G; 98 T;

Query Match 100.0%; Score 26; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgtagtagtgagtgctgcgcgcct 26
    |||||
Db 54 GCGTTAGTAGTGAGTGCTGCAGCCT 79

RESULT 4
Q12239
ID Q12239 standard; DNA; 504 BP.
AC Q12239;
DT 06-SEP-1991 (first entry)
DE Clone 164/137 encoding PT-NANBH virus antigenic portion.
KW Post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 308..504
FT /*tag= a
FT /product= start of PT-NANBH polyprotein
PN GB2239245-A.
PD 26-JUN-1991.
PR 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI; 91-187584/26.
DR P-PSDB; R12597.
PT Post-transfusional non-A non-B hepatitis poly-peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 71-72; 108pp; English.
CC This sequence probably encodes viral structural proteins of the
CC PT-NANBH viral genome having antigenic properties. It was
CC isolated from serum of humans infected by the virus.
CC See also Q12236-8 and Q12240-Q12242.
SQ Sequence 504 BP; 106 A; 147 C; 153 G; 98 T;

Query Match 100.0%; Score 26; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgtagtagtgagtgctgcgcgcct 26
    |||||
Db 54 GCGTTAGTAGTGAGTGCTGCAGCCT 79

RESULT 5
Q14083
ID Q14083 standard; DNA; 202 BP.
AC Q14083;
DT 03-JAN-1992 (first entry)
DE HCV-T (1-202).
KW Epitope; PCR; diagnosis; ss.
OS Hepatitis C virus.
EN WO9114779-A.
PD 03-OCT-1991.
PR 28-MAR-1991; J00405.
PR 28-MAR-1990; JP-080185.
PR 13-JUN-1990; JP-154230.
PR 14-JUN-1990; JP-153979.
PR 09-NOV-1990; JP-305795.
PA (MITK) MITSUI TOATSU CHEM INC.
PI Takada T, Enomoto N, Date T, Nakao T;
DR WPI; 91-310579/42.
PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
PT of hepatitis C virus infection via polymerase chain reaction
PS Disclosure; Fig 1(1); 79pp; Japanese.
CC The nucleotide sequences represented in Q14076-86 and Q14767-71
CC encode epitopes from structural, non-structural and 5' untranslated
CC domains of hepatitis C virus. The sequences are used for accurate
CC and simple diagnosis and typing of HCV infection, using PCR
CC amplification techniques.
SQ Sequence 202 BP; 39 A; 61 C; 61 G; 41 T;

Query Match 100.0%; Score 26; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgtagtagtgagtgctgcgcgcct 26
    |||||
Db 54 GCGTTAGTAGTGAGTGCTGCAGCCT 79

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Q12242
ID Q12242 standard; DNA; 2116 BP.
AC Q12242;
DT 17-SEP-1991 (first entry)
DE Encodes PT-NANBH viral structural and non-structural proteins.
KW Post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 308..2116
FT /*tag= a
PN GB2239245-A.
PD 26-JUN-1991.
PR 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI; 91-187584/26.
DR P-PSDB; R12600.
PT Post-transfusional non-A non-B hepatitis poly-peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 83-87; 108pp; English.
CC This sequence is thought to encode viral structural and non-
CC structural proteins of the PT-NANBH viral genome which are antigenic.
CC It was isolated from human serum infectious for the virus.
CC See also Q12236-41.
SQ Sequence 2116 BP; 392 A; 650 C; 624 G; 450 T;

Query Match 100.0%; Score 26; DB 1; Length 2116;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgtagtagtgagtgctgcgcgcct 26
    |||||
Db 54 GCGTTAGTAGTGAGTGCTGCAGCCT 79

RESULT 5
Q14083
ID Q14083 standard; DNA; 202 BP.
AC Q14083;
DT 03-JAN-1992 (first entry)
DE HCV-T (1-202).
KW Epitope; PCR; diagnosis; ss.
OS Hepatitis C virus.
EN WO9114779-A.
PD 03-OCT-1991.
PR 28-MAR-1991; J00405.
PR 28-MAR-1990; JP-080185.
PR 13-JUN-1990; JP-154230.
PR 14-JUN-1990; JP-153979.
PR 09-NOV-1990; JP-305795.
PA (MITK) MITSUI TOATSU CHEM INC.
PI Takada T, Enomoto N, Date T, Nakao T;
DR WPI; 91-310579/42.
PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
PT of hepatitis C virus infection via polymerase chain reaction
PS Disclosure; Fig 1(1); 79pp; Japanese.
CC The nucleotide sequences represented in Q14076-86 and Q14767-71
CC encode epitopes from structural, non-structural and 5' untranslated
CC domains of hepatitis C virus. The sequences are used for accurate
CC and simple diagnosis and typing of HCV infection, using PCR
CC amplification techniques.
SQ Sequence 202 BP; 39 A; 61 C; 61 G; 41 T;

Query Match 100.0%; Score 26; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcgtagtagtgagtgctgcgcgcct 26
    |||||
Db 54 GCGTTAGTAGTGAGTGCTGCAGCCT 79

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QY 1 gcgttagtatgagtcgtgcagcct 26
 |||||
 Db 45 GCCTTAGTATGAGTCGTCGACGCT 70

RESULT 6

Q14084 Q14084 standard; DNA; 202 BP.
 AC Q14084;
 DT 03-JAN-1992 (first entry)
 DE HCV-1 (1-202).
 KW Epitope; PCR; diagnosis: ss.
 OS Hepatitis C virus.
 PN W09114779-A.
 PD 03-OCT-1991.
 PF 28-MAR-1991; J00405.
 PR 28-MAR-1990; JP-080185.
 PR 13-JUN-1990; JP-154230.
 PR 14-JUN-1990; JP-153979.
 PR 09-NOV-1990; JP-305795.
 PA (MIRK) MIRSUI TOATSU CHEM INC.
 PI Takada T, Enomoto N, Date T, Nakao T;
 WPI; 91-310579/42.
 PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
 of hepatitis C virus infection via polymerase chain reaction
 PS Disclosure: Fig 1(I): 79pp; Japanese.
 CC The nucleotide sequences represented in Q14076-86 and Q14767-71
 encode epitopes from structural, non-structural and 5' untranslated
 domains of hepatitis C virus. The sequences are used for accurate
 CC and simple diagnosis and typing of HCV infection, using PCR
 CC amplification techniques.
 SQ Sequence 202 BP; 41 A; 60 C; 60 G; 41 T;

Query Match 100.0%; Score 26; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgttagtatgagtcgtgcagcct 26
 |||||
 Db 45 GCCTTAGTATGAGTCGTCGACGCT 70

RESULT 7

Q15363 Q15363 standard; DNA; 1863 BP.
 AC Q15363;
 DT 17-MAR-1992 (first entry)
 DE Fragment of NANB hepatitis virus strain HC-J4.
 KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
 OS Polymerase chain reaction; ss.
 OS Hepatitis C virus.
 FH Key Location/Qualifiers
 FT 5'utr 1..324
 FT /*tag= a
 FT /*tag= b

RESULT 8

Q15362 Q15362 standard; CDNA; 1863 BP.
 AC Q15362;
 DT 17-MAR-1992 (first entry)
 DE Fragment of NANB hepatitis virus strain HC-J4.
 KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
 OS Polymerase chain reaction; ss.
 OS Hepatitis C virus.
 FH Key Location/Qualifiers
 FT 5'utr 1..324
 FT /*tag= a
 FT /*tag= b

CC A study of the deduced sequence suggested that the CDS encodes NANBH
 virus core proteins. Primers for detecting NANB hepatitis virus were
 CC designed based on the HC-J4 sequence.
 SQ Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T;

Query Match 100.0%; Score 26; DB 1; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgttagtatgagtcgtgcagcct 26
 |||||
 Db 71 GCCTTAGTATGAGTCGTCGACGCT 96

RESULT 9

Q15362 Q15362 standard; CDNA; 1863 BP.
 AC Q15362;
 DT 17-MAR-1992 (first entry)
 DE Fragment of NANB hepatitis virus strain HC-J4.
 KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
 OS Polymerase chain reaction; ss.
 OS Hepatitis C virus.
 FH Key Location/Qualifiers
 FT 5'utr 1..324
 FT /*tag= a
 FT /*tag= b
 FT EP-461863-A.
 PD 18-DEC-1991.
 PF 11-JUN-1991; 305270.
 PR 12-JUN-1990; JP-153402.
 PA (IMMU-) IMMUNO JAPAN INC.
 PI Okamoto H, Ogikubo Y;
 WPI; 91-370834/51.
 DR Oligo-nucleotide primers - derived from and used to detect and
 PT diagnose non-A, non-B hepatitis virus
 PS Claim 1; Page 7; 23pp; English.
 CC NANB hepatitis virus strain HC-J4 was isolated from a plasma sample
 of a Japanese blood donor who tested positive for HCV antibody. RNA
 CC was isolated from the sample and reverse transcribed into cDNA. The
 CC 513 amino acids encoded by the CDS were determined but are not given
 CC in the specification (and hence are not included in A-Geneseq). A
 CC study of the deduced sequence suggested that the CDS encodes NANBH
 CC virus core proteins. Primers for detecting NANB hepatitis virus were
 CC designed based on the HC-J4 sequence.
 SQ Sequence 1863 BP; 347 A; 581 C; 533 G; 402 T;

Query Match 100.0%; Score 26; DB 1; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgttagtatgagtcgtgcagcct 26
 |||||
 Db 71 GCCTTAGTATGAGTCGTCGACGCT 96

RESULT 9

Q21829 Q21829 standard; CDNA; 9416 BP.
 AC Q21829;
 DT 01-MAY-1992 (first entry)
 DE Non-A, non-B viral genome.
 KW NANBH; vaccine; immunodiagnosis; antigen; antibody; ds.
 OS Non-A, non-B hepatitis virus.
 FH Key Location/Qualifiers
 FT cds 333..677
 FT /*tag= a
 FT /*product= c
 FT /*note= "core protein"
 FT cds 678..905

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FT FT      /tag= b
FT FT      /product= M
FT FT      /note= "matrix protein"
FT FT      906..1499
FT FT      /tag= c
FT FT      /product= E
FT FT      /note= "envelope protein"
FT FT      1500..2519
FT FT      /tag= d
FT FT      /product= NS1
FT FT      /tag= e
FT FT      /product= NS2
FT FT      3351..5177
FT FT      /tag= f
FT FT      /product= NS3
FT FT      5178..5918
FT FT      /tag= g
FT FT      /product= NS4a
FT FT      5919..6371
FT FT      /tag= h
FT FT      /product= NS4b
FT FT      6372..9365
FT FT      /tag= i
FT FT      /product= NS5
FT FT      EP-464287-A.
FT FT      08-JAN-1992. 314371.
FT FT      28-DEC-1990. 314371.
FT FT      25-JUN-1990. JP-167466.
FT FT      31-AUG-1990. JP-230921.
FT FT      09-NOV-1990. JP-305605.
FT FT      (OSAU ) Osaka University.
FT FT      Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
FT FT      WPI: 92-009617/02.
FT FT      P-PSDB: R20091.
FT FT      Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
FT FT      diagnostics and screening agents for NANBV, and to remove NANBV from
FT FT      blood.
FT FT      Claim 1: Fig 2: 89pp; English.
FT FT      The sequence was obtd. from several overlapping "BK" cDNA clones
FT FT      obtd. by "gene walking" using a cDNA clone isolated from a library
FT FT      prep'd. from NANBV RNA. The DNA and fragments of it can be used
FT FT      for the detection of the presence of NANBV by hybridisation or PCR.
FT FT      Antigenic polypeptides encoded by the sequence can be used as
FT FT      immunoassay reagents, for screening donated blood, and as immuno-
FT FT      gens for vaccine prodn. Antibodies raised to the peptides can be
FT FT      used in immunoassays to detect or quantify NANBV antigens in liver
FT FT      tissue and blood. Preferred polypeptides are encoded by the
FT FT      following nucleotides: 333-422, -677, or -6371; 474-563; 678-905;
FT FT      906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
FT FT      2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5919-
FT FT      6371; and 6372-9372. The sequence is also disclosed in EP-463848
FT FT      in which a virus particle contg. antigens encoded by the sequence
FT FT      is claimed, as well as expression vectors contg. the sequence.
FT FT      See Q20268 for details of this specification.
FT FT      Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;
SQ

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RESULT 10

Q20268

ID Q20268 standard: cDNA; 9416 BP.

AC Q20268;

DT 01-MAY-1992 (first entry)

DE Non-A, non-B viral genome.

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QY 1 gcgttagatgagtgctgcagcct 26
    |||||
DB 79 GCCTTAGTATGAGTGCTGCAGCCT 104

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Query Match 100.0%; Score 26; DB 1; Length 9416;
 Best Local Similarity 100.0%; Pred. No. 0.00058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KW NANBV; vaccine; immunodiagnosis; antigen; antibody; ds.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT FT      333..677
FT FT      /tag= a
FT FT      /product= C
FT FT      /note= "core protein"
FT FT      678..905
FT FT      /tag= b
FT FT      /product= M
FT FT      /note= "matrix protein"
FT FT      906..1499
FT FT      /tag= c
FT FT      /product= E
FT FT      /note= "envelope protein"
FT FT      1500..2519
FT FT      /tag= d
FT FT      /product= NS1
FT FT      /tag= e
FT FT      /product= NS2
FT FT      3351..5177
FT FT      /tag= f
FT FT      /product= NS3
FT FT      5178..5918
FT FT      /tag= g
FT FT      /product= NS4a
FT FT      5919..6371
FT FT      /tag= h
FT FT      /product= NS4b
FT FT      6372..9365
FT FT      /tag= i
FT FT      /product= NS5
FT FT      EP-463848-A.
FT FT      02-JAN-1991. 305717.
FT FT      25-JUN-1991. JP-167466.
FT FT      31-AUG-1990. JP-230921.
FT FT      09-NOV-1990. JP-305605.
FT FT      28-DEC-1990. US-635451.
FT FT      08-MAY-1991. JP-132090.
FT FT      14-MAY-1991. JP-138493.
FT FT      (OSAU ) Osaka University.
FT FT      Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
FT FT      WPI: 92-009412/02.
FT FT      P-PSDB: R20111.
FT FT      Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
FT FT      diagnostics and screening agents for NANBV, and to remove NANBV from
FT FT      blood.
FT FT      Disclosure: Fig 2: 89pp; English.
FT FT      The sequence was obtd. from several overlapping "BK" cDNA clones
FT FT      obtd. by "gene walking" using a cDNA clone isolated from a library
FT FT      prep'd. from NANBV RNA. The DNA and fragments of it can be used
FT FT      for the detection of the presence of NANBV by hybridisation or PCR.
FT FT      Antigenic polypeptides encoded by the sequence can be used as
FT FT      immunoassay reagents, for screening donated blood, and as immuno-
FT FT      gens for vaccine prodn. Antibodies raised to the peptides can be
FT FT      used in immunoassays to detect or quantify NANBV antigens in liver
FT FT      tissue and blood. Preferred polypeptides are encoded by the
FT FT      following nucleotides: 333-422, -677, or -6371; 474-563; 678-905;
FT FT      906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
FT FT      2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5919-
FT FT      6371; and 6372-9372. The sequence is also disclosed in EP-464287
FT FT      in which it is claimed. See Q21829 for details of this specifi-
FT FT      cation.
FT FT      Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;
SQ

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Query Match 100.0%; Score 26; DB 1; Length 9416;
 Best Local Similarity 100.0%; Pred. No. 0.00058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgttagatgagtgctgcagcct 26

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Db 79 GCGTTAGTAGTGAGTGCTGTCGAGCCT 104
|||||
RESULT 11
Q20940
ID Q20940 standard; DNA; 807 BP.
AC Q20940;
DE 13-MAY-1992 (first entry)
DT PCR-generated fragment of Hepatitis C virus cDNA from clone M642.
KW Non-A, non-B hepatitis virus; NANBHV; ss.
OS Hepatitis C virus.
PN EP-469348-A.
PD 05-FEB-1992.
PF 09-JUL-1991; 111413.
PR 11-JUL-1990; JP-183512.
PR 18-DEC-1990; JP-412177.
PR 30-JAN-1991; JP-029364.
PR 14-FEB-1991; JP-042855.
PA (SHIO ) SHIONOGI KK.
PI Kamada T, Hayashi N, Mita E, Ueda K;
DR WPI; 92-042764/06.
PT cDNA sequence for detection of hepatitis C - isolated from liver
of HCV-antibody positive patients for use in polymerase chain
PT reaction
PS Claim 1: Page 23; 26pp; English.
CC RNA was extracted from the liver of a patient with liver cancer.
CC cDNA was prepared from the RNA using an anti-sense primer (see
Q20941) and MMuLV reverse transcriptase. The cDNA was amplified by
CC the PCR method using the same anti-sense primer with a sense primer
CC (see Q20942). The PCR product was subjected to a second PCR
CC amplification using a different primer pair (see Q20943 and
Q20944). The PCR product was electrophoresed and a single band of
CC the expected size was cut out. DNA was extracted from the gel and
CC cloned in pBluescript II SK(plus). The recombinant vector was used
CC to transform competent E.coli XL-1-B. DNA was extracted from the
CC transformants, digested with BamHI and EcoRI and allowed to migrate
CC on a gel. Positive clones were selected based on the size of the
CC restriction fragments. DNA from one of the positive clones (M642)
CC was sequenced.
SQ Sequence 807 BP; 148 A; 253 C; 255 G; 151 T;

Query Match 100.0%; Score 26; DB 1; Length 807;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgttagtagtgagtgctgcgagcct 26
|||||
Db 73 GCGTTAGTAGTGAGTGCTGTCGAGCCT 98
|||||

RESULT 12
Q21744
ID Q21744 standard; DNA; 9400 BP.
AC Q21744;
DE 22-JUN-1992 (first entry)
DT Compiled HCV cDNA.
KW HCV1; serum; gtl1; oligomer; target; ds.
OS Hepatitis C virus 1.
FH Key Location/Qualifiers
FT cds 341..9373
FT /*tag= a
FT /label= polyprotein
FT 357..386
FT /*tag= b
FT /label= target_region
FT /note= "see CC"
FT misc_feature 390..419
FT /*tag= c
FT /label= target_region
FT /note= "see CC"
FT misc_feature 423..452

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FT /*tag= d
FT /label= target_region
FT /note= "see CC"
FT 456..485
FT /*tag= e
FT /label= target_region
FT /note= "see CC"
FT 489..518
FT /*tag= f
FT /label= target_region
FT /note= "see CC"
FT 552..581
FT /*tag= g
FT /label= target_region
FT /note= "see CC"
FT 583..612
FT /*tag= h
FT /label= target_region
FT /note= "see CC"
FT 616..645
FT /*tag= i
FT /label= target_region
FT /note= "see CC"
FT 673..702
FT /*tag= j
FT /label= target_region
FT /note= "see CC"
FT 706..735
FT /*tag= k
FT /label= target_region
FT /note= "see CC"
FT 739..768
FT /*tag= l
FT /label= target_region
FT /note= "see CC"
FT 798..827
FT /*tag= m
FT /label= target_region
FT /note= "see CC"
PN W09202642-A.
PD 20-FEB-1992.
PF 12-AUG-1991; U05728.
PR 10-AUG-1990; US-566209.
PA (CHIR-) CHIRON CORP.
PI Houghton M, Choo QL, Kuo G, Weiner AJ, Urdea MS, Irvine BD;
PI Kolberg JA;
PI WPI; 92-080094/10.
DR P-PSDB; R21519.
DT Reagents for isolating, amplifying and detecting HCV
PT polynucleotide(s) - used to monitor spread of blood-borne non-A,
PT non-B hepatitis virus infection and screen blood samples for
PT virus
PS Disclosure; Fig 1; 67pp; English.
CC The sequence is a composite of HCV cDNA from HCV1, a prototypic
CC HCV. The sequence is based upon sequence information derived from
CC a no. of HCV cDNA clones, which were isolated from a no. of HCV
CC cDNA libraries, including the "c" library present in lambda gt11
CC (ATCC No.40394), and from human serum. The HCV cDNA clones
CC were isolated by methods described in W09014436.
CC The clones from which the sequence was derived are 5'clone32,
CC b114a, 18g, ag30a, CA290a, CA216a, p114a, CA167b, CA156a,
CC CA84a, CA59a, K9-1 (also called K9-1), 26j, 13i, 12f, 14i, 11b, 7f,
CC 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g,
CC 39c, 35f, 19g, 26g, 15e, b5a, 16jh, 6k and p131jh.
CC The target regions indicated in the features are listed in claim 1,
CC page 49. Oligomers are provided which are complementary to these
CC target regions and used in the detection of an HCV sequence in an
CC analyte.
SQ Sequence 9400 BP; 1885 A; 2860 C; 2671 G; 1984 T;

Query Match 100.0%; Score 26; DB 1; Length 9400;
Best Local Similarity 100.0%; Pred. No. 0.00058;

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 gcgttagtgatgctgcgcagcct 26
    |||||
Db 88 GCGTTAGTAGTGCTGCTGAGCCT 113

RESULT 13
Q22871
ID Q22871 standard; DNA; 9416 BP.
AC Q22871;
DE 07-JUL-1992 (first entry)
DE NANBV Hutch c59 isolate genome.
KW Hepatitis C virus; non-A non-B virus; HCV-Hc59; primers;
KW probes; vaccine; ss.
OS NANBV Hutch c59 isolate.
FH Key Location/Qualifiers
FT cds 342..9377
FT /tag= a
FT /label= viral_genome
FT misc_feature 1..12
FT /tag= b
FT /note= "not confirmed as HCV-Hc59 sequence"
FT misc_feature 9397..9416
FT /tag= c
FT /note= "not confirmed as HCV-Hc59 sequence"
FT repeat_unit 7..12
FT /tag= d
FT /rpt_type= 1
FT repeat_unit 42..47
FT /tag= e
FT /rpt_type= 1
FT repeat_unit 23..28
FT /tag= f
FT /rpt_type= 2
FT repeat_unit 38..43
FT /tag= g
FT /rpt_type= 2
FT repeat_unit 128..135
FT /tag= j
FT /rpt_type= 3
FT repeat_unit 315..322
FT /tag= k
FT /rpt_type= 3
FT repeat_unit 315..322
FT /tag= l
FT /rpt_type= 3
FT repeat_unit 9231..9237
FT /tag= m
FT /rpt_type= 4
FT repeat_unit 9245..9251
FT /tag= n
FT /rpt_type= 4
FT repeat_unit 9256..9262
FT /tag= o
FT /rpt_type= 4
FT repeat_unit 9248..9253
FT /tag= p
FT /rpt_type= 5
FT repeat_unit 9221..9226
FT /tag= q
FT /rpt_type= 5
FT repeat_unit 9227..9232
FT /tag= r
FT /rpt_type= 5
FT misc_difference 351..353
FT /tag= s
/label= AAT
/note= "or ATT according to Seq No 1 (Q22838), see CC"
/seq= t
/label= AAT
/note= "or GAT according to Seq No 1 (Q22838), see CC"
/seq= u
/product= NANBV_structural_proteins
/seq= "Seq No 1 (Q22838)"
/seq= v
/label= capsid
/seq= w
/label= envelope_protein
/seq= x
/label=
/seq= "pref. capsid antigen"
/seq= y
/seq= "pref. capsid antigen"
/seq= z
/seq= "pref. capsid antigen"
/seq= aa
/seq= "pref. capsid antigen"
/seq= ab
/seq= "pref. capsid antigen"
/seq= ac
/seq= "pref. envelope antigen"
/seq= ad
/seq= "pref. envelope antigen"
/seq= ae
/label= V.variable_region
/seq= af
/label= V1.variable_region
/seq= ag
/label= V2.variable_region
/seq= ah
/label= V3.variable_region
/seq= ai
/seq= "pref. V fragment"
/seq= aj
/seq= "pref. V1 fragment"
/seq= ak
/seq= "pref. V2 fragment"
/seq= al
/seq= "pref. V2 fragment"
/seq= am
/label= oligonucleotide_693
/seq= "used in NANBV cloning"
/seq= an
/label= oligonucleotide_694
/seq= "used in NANBV cloning"
/seq= ao
/label= oligonucleotide_691

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FT misc_rna /note= "used in NANBV cloning"
FT 697..715
FT FT /*tag= ap
FT /label= oligonucleotide_14
FT /note= "used in NANBV cloning"
FT 702..718
FT FT /*tag= ag
FT /label= oligonucleotide_15
FT /note= "used in NANBV cloning"
FT /*tag= ar
FT /label= oligonucleotide_18
FT /note= "used in NANBV cloning"
FT W09203458-A.
FT PD 05-MAR-1992
FT PN U06037.
FT PF 23-AUG-1991; US-573643.
FT PR 25-AUG-1990; US-616369.
FT PR 21-NOV-1990; US-616369.
FT PA (NYBL-) NEW YORK BLOO DCENT.
FT PA (PHAA-) PHARMACIA GENETIC ENG INC.
FT PI Zebedee S. Inchauspe G, Nasofe MS, Prince AM;
FT DR WPI: 92-096821/12.
FT DR P-PSDB; R22154.
FT PT Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis
FT PT virus - obtd. Hutch C59 subgroup encoding polypeptide(s), useful
FT PT as vaccines, and immuno reactive Abs for diagnosis of virus
FT PS Disclosure: Page 159-173; 225pp; English.
FT CC One Hutch strain (HCV-H) of NANBV, designated the Hutch c59 isolate
FT CC (HCV-Hc59) was propagated through passage in animals and the
FT CC entire viral genome was cloned and sequenced.
FT CC The sequence in Q22838 (tag u) comprises two bases, indicated in
FT CC the features, which differ from the sequence represented here.
FT CC Two more oligonucleotides used in NANBV cloning are shown in
FT CC Q22838, and one in Q22859.
FT CC The encoded proteins and peptides (see features) and antibodies
FT CC against them are useful for the prepn. of vaccines and inoculums
FT CC against NANBV and in immunological assays for detection of viral
FT CC infection. The nucleic acid may be used to detect the presence of
FT CC NANBV DNA.
FT CC Nucleotide sequences used in the prodn. of polynucleotides are
FT CC selected from the V, VI, V2 and V3 variable region. The regions
FT CC indicated in the features encode peptides contg. the greatest amt. of
FT CC diversity when compared to known HCV isolates. The polynucleotides
FT CC may be used as primers, probes, or a nucleic acids
FT CC Sequence 9416 BP; 1879 A; 2849 C; 2683 G; 2005 T;
FT SQ
Query Match 100.0%; Score 26; DB 1; Length 9416;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcgttagtatgagtcgtgcagcct 26
DB 88 GCGTTAGTATGAGTCGTGCAGCCT 113
RESULT 14
Q24457
ID Q24467 standard; DNA; 1880 BP.
AC Q24467;
DT 09-NOV-1992 (first entry)
DE NANB hepatitis virus strain HC-J4 genome.
KW non-A, non-B hepatitis virus; NANBV; PCR; amplification
KW polymerase chain reaction; vaccine; antibody; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 342..1880
FT /*tag= a
FT /label= HC-J4
FT EP-485209-A.
FT PD 13-MAY-1992.
FT PN 07-NOV-1991; 310297.
FT PR 08-NOV-1990; JP-304405.
FT PA (IMMO-) IMMUNO JAPAN INC.
FT PI Nakamura T, Okamoto H;
FT DR WPI: 92-160959/20.
FT DR P-PSDB; R24086.
FT PT Recombinant cDNA of NANBV virus strain HC-J5 and corresp.
FT PT peptides - useful for diagnosis and in vaccines and immunological
FT PT pharmaceuticals
FT PS Disclosure: Page 8; 42pp; English.
FT CC This sequence is the genome of the non-A, non-B hepatitis virus
FT CC (NANBV) strain HC-J1. This sequence was derived by amplification
FT CC by polymerase chain reaction. The nucleotide sequences derived from
FT CC this amplification can be used to detect NANBV infection which could
FT CC not be detected by conventional methods. The detection kits allow
FT CC highly specific and sensitive detection at an early phase of
FT CC infection. The polypeptide product of this coding sequence can be used
FT CC for the manufacture of vaccines and immunological pharmaceuticals
FT CC and also to produce antibodies specific to NANBV.
FT SQ Sequence 1880 BP; 349 A; 582 C; 546 G; 403 T;
Query Match 100.0%; Score 26; DB 1; Length 1880;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcgttagtatgagtcgtgcagcct 26
DB 88 GCGTTAGTATGAGTCGTGCAGCCT 113

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PA (IMMO-) IMMUNO JAPAN INC.
PI Nakamura T, Okamoto H;
DR WPI: 92-160959/20.
DR P-PSDB; R24087.
PT Recombinant cDNA of NANBV virus strain HC-J5 and corresp.
PT peptides - useful for diagnosis and in vaccines and immunological
PT pharmaceuticals
PS Disclosure: Page 11; 42pp; English.
CC This sequence is the genome of the non-A, non-B hepatitis virus
CC (NANBV) strain HC-J4. This sequence was derived by amplification
CC by polymerase chain reaction. The nucleotide sequences derived from
CC this amplification can be used to detect NANBV infection which could
CC not be detected by conventional methods. The detection kits allow
CC highly specific and sensitive detection at an early phase of
CC infection. The polypeptide product of this coding sequence can be used
CC for the manufacture of vaccines and immunological pharmaceuticals
CC and also to produce antibodies specific to NANBV.
SQ Sequence 1880 BP; 333 A; 593 C; 556 G; 398 T;
Query Match 100.0%; Score 26; DB 1; Length 1880;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcgttagtatgagtcgtgcagcct 26
DB 88 GCGTTAGTATGAGTCGTGCAGCCT 113
RESULT 15
Q24466
ID Q24466 standard; DNA; 1880 BP.
AC Q24466;
DT 09-NOV-1992 (first entry)
DE NANB hepatitis virus strain HC-J1 genome.
KW non-A, non-B hepatitis virus; NANBV; PCR; amplification
KW polymerase chain reaction; vaccine; antibody; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 342..1880
FT /*tag= a
FT /label= HC-J1
FT EP-485209-A.
FT PD 13-MAY-1992.
FT PN 07-NOV-1991; 310297.
FT PR 08-NOV-1990; JP-304405.
FT PA (IMMO-) IMMUNO JAPAN INC.
FT PI Nakamura T, Okamoto H;
FT DR WPI: 92-160959/20.
FT DR P-PSDB; R24086.
FT PT Recombinant cDNA of NANBV virus strain HC-J5 and corresp.
FT PT peptides - useful for diagnosis and in vaccines and immunological
FT PT pharmaceuticals
FT PS Disclosure: Page 8; 42pp; English.
FT CC This sequence is the genome of the non-A, non-B hepatitis virus
FT CC (NANBV) strain HC-J1. This sequence was derived by amplification
FT CC by polymerase chain reaction. The nucleotide sequences derived from
FT CC this amplification can be used to detect NANBV infection which could
FT CC not be detected by conventional methods. The detection kits allow
FT CC highly specific and sensitive detection at an early phase of
FT CC infection. The polypeptide product of this coding sequence can be used
FT CC for the manufacture of vaccines and immunological pharmaceuticals
FT CC and also to produce antibodies specific to NANBV.
FT SQ Sequence 1880 BP; 349 A; 582 C; 546 G; 403 T;
Query Match 100.0%; Score 26; DB 1; Length 1880;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcgttagtatgagtcgtgcagcct 26
DB 88 GCGTTAGTATGAGTCGTGCAGCCT 113

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Search completed: November 23, 1999, 13:58:51
Job time: 6678 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 23, 1999, 13:58:51 ; Search time 70.49 Seconds
(without alignments)
70.987 Million cell updates/sec

Title: US-09-031-087-2
Perfect score: 20
Sequence: 1 ggtgcacggctcagagacc 20

Scoring table: IDENTITY_NUC
Searched: 31158586qs, 125096042 residues
Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	20	100.0	9185	1	Q05956	Sense strand of th
C 2	20	100.0	9185	1	Q10566	Hepatitis C virus
C 3	20	100.0	504	1	Q12239	Clone 164/137 enco
C 4	20	100.0	2116	1	Q12242	Encodes PT-NANBH v
C 5	20	100.0	1863	1	Q15363	Fragment of NANBH h
C 6	20	100.0	1863	1	Q15362	Fragment of NANBH h
C 7	20	100.0	9416	1	Q21829	Non-A, non-B viral
C 8	20	100.0	9416	1	Q20268	Non-A, non-B viral
C 9	20	100.0	807	1	Q20940	PCR-generated frag
C 10	20	100.0	9416	1	Q22871	NANBH Hutch c59 is
C 11	20	100.0	1880	1	Q24467	NANBH hepatitis vir
C 12	20	100.0	1886	1	Q24468	NANBH hepatitis vir
C 13	20	100.0	1880	1	Q24466	NANBH hepatitis vir
C 14	20	100.0	1682	1	Q27159	NANBH hepatitis vir
C 15	20	100.0	117	1	Q27657	Oligomer GBL corre
C 16	20	100.0	2540	1	Q29628	Hepatitis C virus
C 17	20	100.0	2540	1	Q29627	Hepatitis C virus
C 18	20	100.0	1885	1	Q29629	Hepatitis C virus
C 19	20	100.0	2551	1	Q29630	Hepatitis C virus
C 20	20	100.0	252	1	Q31071	HCV-1 genotype GII
C 21	20	100.0	252	1	Q31066	HCV-1 genotype GI
C 22	20	100.0	252	1	Q31067	HCV-1 genotype GI
C 23	20	100.0	252	1	Q31068	HCV-1 genotype GI
C 24	20	100.0	252	1	Q31069	HCV-1 genotype GI
C 25	20	100.0	252	1	Q31070	HCV-1 genotype GI
C 26	20	100.0	483	1	Q32446	HCV core-envelope
C 27	20	100.0	483	1	Q32447	HCV core-envelope
C 28	20	100.0	483	1	Q32453	HCV core-envelope
C 29	20	100.0	9379	1	Q36209	Composite cDNA for
C 30	20	100.0	9472	1	Q32282	Korean hepatitis C
C 31	20	100.0	9589	1	Q38218	NANBH virus strain
C 32	20	100.0	9391	1	Q38959	Hepatitis C virus
C 33	20	100.0	9405	1	Q40426	Hepatitis C virus
C 34	20	100.0	1734	1	Q40425	Full-length Hepati
C 35	20	100.0	1734	1	Q40427	Hepatitis C virus
C 36	20	100.0	1734	1	Q40434	Hepatitis C virus
C 37	20	100.0	1734	1	Q40436	Hepatitis C virus
C 38	20	100.0	1734	1	Q40437	Hepatitis C virus
C 39	20	100.0	1734	1	Q40438	Hepatitis C virus
C 40	20	100.0	1734	1	Q40439	Hepatitis C virus
C 41	20	100.0	29	1	Q43112	HCV 5' NCR antisens
C 42	20	100.0	2540	1	Q43889	NANBH hepatitis vir
C 43	20	100.0	1885	1	Q43890	NANBH hepatitis vir

C 44 20 100.0 2551 1 Q43891 NANB hepatitis vir
C 45 20 100.0 1270 1 V60668 Fragment #1 isolat

ALIGNMENTS

```
RESULT 1
Q05956/c
ID Q05956 standard; DNA; 9185 BP.
AC Q05956;
DE 23-JAN-1991 (first entry)
DT Sense strand of the compiled Hepatitis C virus cDNA sequence.
KW Hepatitis C virus (HCV); antiviral agent; ss.
OS Hepatitis C virus.
FH Key
FT cds Location/Qualifiers
   320..9185
   /*tag= a
FT misc_rna 1..1667
   /*tag= b
FT /*note="epitope within this region is claimed"
FT misc_rna 8978..9185
   /*tag= c
FT /*note="encodes an epitope that is claimed"
PN EP-388232-A.
PD 19-SEP-1990.
PF 16-MAR-1990; 302866.
PR 17-MAR-1989; US-325338.
PR 20-APR-1989; US-341334.
PR 18-MAY-1989; US-355002.
PA (CHIR-) CHIRON CORP.
PI Houghton M, Choo QL, Kuo G.;
DR P-PSDB; R08124.
PT Hepatitis C virus DNA - used for producing probes,
   polypeptide(s), antibodies and anti-sense polynucleotide(s) for
   diagnosis and therapy.
PS Disclosure; Fig 17; 83pp; English.
CC HCV cDNA libraries were constructed using pooled serum from a
   chimpanzee with chronic HCV infection. A lambda gt11 library was
   screened with probes derived from previously isolated clones. The
   ORF is derived from the overlapping clones bil4a, ag30a, CA205a,
   CA290a, CA216a, pi4a, CA167b, CA156e, CA84a, CA59a, K9-1, 26j, 13i,
   12f, 14i, 11b, 7f, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c,
   14c, 8f, 33f, 33g, 39c, 35f, 19g, 26g, 15e, b5a and 16jh. These
   clones extend the sequence of the HCV genome reported in EP-318216.
   The upstream region from nucleotides 319 to +1348 (=1-1667 in this
   file) is covered by clones bil4a, 18g, ag30a, CA205a, CA290a,
   CA216a, pi4a, CA167b, CA156e, CA84a and CA59a; nucleotides
   8659-8866 (=8978-9185 in this file) are covered by clones b5a and
   16jh.
CC See also Q05955.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;
```

Query Match 100.0%; Score 20; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtgcacggctcagagacc 20
|||||
Db 319 GGTGCACGGCTCAGAGACC 300

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RESULT 2
Q10566/c
ID Q10566 standard; DNA; 9185 BP.
AC Q10566;
DE 29-APR-1991 (first entry)
DT Hepatitis C virus strain 1 DNA.
KW Hepatitis C virus; HCV-1; non-A, non-B hepatitis; HCV antigen;
   viral infections; ss.
OS Hepatitis C virus.
```

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PN EP-414475-A.
PD 27-FEB-1991.
PR 21-AUG-1990; 309120.
PR 25-AUG-1989; US-398667.
PA (CHIR-) CHIRON CORP.
PI Weiner AJ, Steimer KS;
DR WPI: 91-059670/09.
PT Cell lines infected with hepatitis C virus - are used as source
PT of antigens for detection of HCV antibodies, for vaccines, and
PT for screening anti-viral agents
PS Disclosure: fig 1; 24pp; English.
CC This is a hepatitis C virus (HCV) composite cDNA sequence, deduced
CC using overlapping clones, a compsn. contg. the antigenic protein
CC encoded by this sequence is useful for detecting anti-HCV anti-
CC bodies (Abs) and for screening an agent which inhibits HCV replic-
CC ation. A cell line infected with this virus can be used as a
CC source of antigens. The antigen is useful for preparing vaccines
CC for treating viral infections. See also Q10567.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;

Query Match 100.0%; Score 20; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtgcacggtctacgagacc 20
    |||||
Db 319 GGTGCACGGTCTACGAGACC 300

RESULT 3
Q12239/C
ID Q12239 standard; DNA; 504 BP.
AC Q12239;
DT 06-SEP-1991 (first entry)
DE Clone 154/137 encoding PT-NANBH virus antigenic portion.
KW post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT 308..504
FT /*tag= a
FT /product= start of PT-NANBH polyprotein
PN GB2239245-A.
PD 26-JUN-1991.
PR 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI: 91-187584/26.
PT Post-transfusional non-A non-B hepatitis poly:peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 71-72; 108pp; English.
CC This sequence probably encodes viral structural proteins of the
CC PT-NANBH viral genome having antigenic properties. It was
CC isolated from serum of humans infected by the virus.
CC See also Q12236-8 and Q12240-Q12242.
SQ Sequence 504 BP; 106 A; 147 C; 153 G; 98 T;

Query Match 100.0%; Score 20; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtgcacggtctacgagacc 20
    |||||
Db 307 GGTGCACGGTCTACGAGACC 288

RESULT 4
Q12242/C
ID Q12242 standard; DNA; 2116 BP.
AC Q12242;
DT 17-SEP-1991 (first entry)
DE Encodes PT-NANBH viral structural and non-structural proteins.
KW post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT 308..2116
FT /*tag= a
FT
PN GB2239245-A.
PD 26-JUN-1991.
PR 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI: 91-187584/26.
PT Post-transfusional non-A non-B hepatitis poly:peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 83-87; 108pp; English.
CC This sequence is thought to encode viral structural and non-
CC structural proteins of the PT-NANBH viral genome which are antigenic.
CC It was isolated from human serum infectious for the virus.
CC See also Q12236-41.
SQ Sequence 2116 BP; 392 A; 650 C; 624 G; 450 T;

Query Match 100.0%; Score 20; DB 1; Length 2116;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtgcacggtctacgagacc 20
    |||||
Db 307 GGTGCACGGTCTACGAGACC 288

RESULT 5
Q15363/C
ID Q15363 standard; DNA; 1863 BP.
AC Q15363;
DT 17-MAR-1992 (first entry)
DE Fragment of NANB hepatitis virus strain HC-J4.
KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
KW polymerase chain reaction; ss.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT 5'utr 1..324
FT /*tag= a
FT 325..1863
FT /*tag= b
PN EP-461863-A.
PD 18-DEC-1991.
PR 11-JUN-1991; 305270.
PR 12-JUN-1990; JP-153402.
PA (IMMU-) IMMUNO JAPAN INC.
PI Okamoto H, Ogikubo Y;
DR WPI: 91-370834/51.
PT Oligo-nucleotide primers - derived from and used to detect and
PT diagnose non-A, non-B hepatitis virus
PS Claim 1; Page 7; 23pp; English.
CC NANB hepatitis virus strain HC-J4 was isolated from a plasma sample
CC of a chimpanzee challenged with NANB hepatitis for infectivity but
CC which tested negative for HCV antibody by Ortho HCV Ab ELISA test.
CC RNA was isolated from the sample and reverse transcribed into cDNA.
CC The 513 amino acids encoded by the CDS were determined but are not
CC given in the specification (and hence are not included in A-Geneseq).
CC A study of the deduced sequence suggested that the CDS encodes NANBH
CC virus core proteins. Primers for detecting NANB hepatitis virus were
CC designed based on the HC-J4 sequence.

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SQ Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T;

Query Match 100.0%; Score 20; DB 1; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0.072;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgacggtctacgagacc 20
 |||||
 DB 324 GGTGACGGTCTACGAGACC 305

RESULT 6

Q15362/C
 ID Q15362 standard; cDNA; 1863 BP.
 AC Q15362;
 DT 17-MAR-1992 (first entry)
 DE Fragment of NANB hepatitis virus strain HC-J1.
 KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
 OS Hepatitis C virus.
 FH Key Location/Qualifiers
 FT 5'utr 1..324
 FT /tag= a
 FT /tag= b
 FT EP-461863-A.
 PD 18-DEC-1991.
 PF 11-JUN-1991; 305270.
 PR 12-JUN-1990; JP-153402.
 PA (IMMU-) IMMUNO-JAPAN INC.
 PI Okamoto H, Ogikubo Y;
 DR WPI-91-370834/51.
 PT Oligo-nucleotide primers - derived from and used to detect and
 PT diagnose non-A, non-B hepatitis virus
 PS Claim 1; Page 7; 23pp; English.
 CC NANB hepatitis virus strain HC-J1 was isolated from a plasma sample
 CC of a Japanese blood donor who tested positive for HCV antibody. RNA
 CC was isolated from the sample and reverse transcribed into cDNA. The
 CC 513 amino acids encoded by the CDS were determined but are not given
 CC in the specification (and hence are not included in A-Geneseq). A
 CC study of the deduced sequence suggested that the CDS encodes NANBH
 CC virus core proteins. Primers for detecting NANB hepatitis virus were
 CC designed based on the HC-J1 sequence.
 SQ Sequence 1863 BP; 347 A; 581 C; 533 G; 402 T;

Query Match 100.0%; Score 20; DB 1; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0.072;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgacggtctacgagacc 20
 |||||
 DB 324 GGTGACGGTCTACGAGACC 305

RESULT 7

Q21829/C
 ID Q21829 standard; cDNA; 9416 BP.
 AC Q21829;
 DT 01-MAY-1992 (first entry)
 DE Non-A, non-B viral genome.
 KW NANBV; vaccine; immunodiagnosis; antigen; antibody; ds.
 OS Non-A, non-B hepatitis virus.
 FH Key Location/Qualifiers
 FT 333..677
 FT /tag= a
 FT /product= C
 FT /note= "core protein"
 FT 678..905
 FT /tag= b
 FT /product= M
 FT /note= "matrix protein"

FT 906..1499
 FT /tag= C
 FT /product= E
 FT /note= "envelope protein"
 FT 1500..2519
 FT /tag= d
 FT /product= NS1
 FT 2520..3350
 FT /tag= e
 FT /product= NS2
 FT 3351..5177
 FT /tag= f
 FT /product= NS3
 FT 5178..5918
 FT /tag= g
 FT /product= NS4a
 FT 5919..6371
 FT /tag= h
 FT /product= NS4b
 FT 6372..9365
 FT /tag= i
 FT /product= NS5

EP-464287-A.
 PN 08-JAN-1992.
 PD 28-DEC-1990; 314371
 PR 25-JUN-1990; JP-167466.
 PR 31-AUG-1990; JP-230921.
 PR 09-NOV-1990; JP-305605.
 PA (OSAU) Osaka University.
 PI Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
 DR WPI; 92-009617/02.
 DR P-PSDB; R20091.
 PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
 PT diagnostics and screening agents for NANBV, and to remove NANBV from
 PT blood.
 PS Claim 1; Fig 2; 89pp; English.
 CC The sequence was obtd. from several overlapping "BK" cDNA clones
 CC obtd. by "gene walking" using a cDNA clone isolated from a library
 CC prep'd. from NANBV RNA. The DNA and fragments of it can be used
 CC for the detection of the presence of NANBV by hybridisation or PCR.
 CC Antigenic polypeptides encoded by the sequence can be used as
 CC immunocassay reagents, for screening donated blood, and as immuno-
 CC gens for vaccine prodn. Antibodies raised to the peptides can be
 CC used in immunoassays to detect or quantify NANBV antigens in liver
 CC tissue and blood. Preferred polypeptides are encoded by the
 CC following nucleotides: 333-422, -677, or -6371; 474-563; 678-905;
 CC 906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
 CC 2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5819-
 CC 6371; and 6372-9372. The sequence is also disclosed in EP-463848
 CC in which a virus particle contg. antigens encoded by the sequence
 CC is claimed, as well as expression vectors contg. the sequence.
 CC See Q20268 for details of this specification.
 SQ Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;

Query Match 100.0%; Score 20; DB 1; Length 9416;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgacggtctacgagacc 20
 |||||
 DB 332 GGTGACGGTCTACGAGACC 313

RESULT 8

Q20268/C
 ID Q20268 standard; cDNA; 9416 BP.
 AC Q20268;
 DT 01-MAY-1992 (first entry)
 DE Non-A, non-B viral genome.
 KW NANBV; vaccine; immunodiagnosis; antigen; antibody; ds.
 OS Non-A, non-B hepatitis virus
 FH Key Location/Qualifiers

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FT 333..677
FT /*tag= a
FT /product= C
FT /note= "core protein"
FT 678..905
FT /*tag= b
FT /product= M
FT /note= "matrix protein"
FT 906..1499
FT /*tag= c
FT /product= E
FT /note= "envelope protein"
FT 1500..2519
FT /*tag= d
FT /product= NS1
FT 2520..3350
FT /*tag= e
FT /product= NS2
FT 3351..5177
FT /*tag= f
FT /product= NS3
FT 5178..5918
FT /*tag= g
FT /product= NS4a
FT 5919..6371
FT /*tag= h
FT /product= NS4b
FT 6372..9365
FT /*tag= i
FT /product= NS5
FT EP-463848-A.
PN 02-JAN-1991.
PD 25-JUN-1991. 305717.
PR 25-JUN-1991; JP-167466.
PR 31-AUG-1990; JP-230921.
PR 09-NOV-1990; JP-305605.
PR 28-DEC-1990; US-635451.
PR 08-MAY-1991; JP-132090.
PR 14-MAY-1991; JP-138493.
PA (OSAU ) Osaka University.
PI Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
DR WPI: 92-009412/02.
DR P-PSDB: R20111.
PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
PT diagnostics and screening agents for NANBV, and to remove NANBV from
PT blood.
PS Disclosure; Fig 2; 89pp; English.
CC The sequence was obtd. from several overlapping "BK" cDNA clones
CC obtd. by "gene walking" using a cDNA clone isolated from a library
CC prepd. from NANBV RNA. The DNA and fragments of it can be used
CC for the detection of the presence of NANBV by hybridisation or PCR.
CC Antigenic polypeptides encoded by the sequence can be used as
CC immunoassay reagents, for screening donated blood, and as immuno-
CC gens for vaccine prodn. Antibodies raised to the peptides can be
CC used in immunoassays to detect or quantify NANBV antigens in liver
CC tissue and blood. Preferred polypeptides are encoded by the
CC following nucleotides: 333-422, -677, or -6371; 474-563; 678-905;
CC 906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
CC 2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5919-
CC 6371; and 6372-9372. The sequence is also disclosed in EP-464287
CC in which it is claimed. See Q21829 for details of this specifi-
CC cation.
CC Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;

Query Match 100.0%; Score 20; DB 1; Length 9416;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgcacggtctacgagacc 20
DB 332 GGTGCACGGTCTACGAGACC 313

FT 333..677
FT /*tag= a
FT /product= C
FT /note= "core protein"
FT 678..905
FT /*tag= b
FT /product= M
FT /note= "matrix protein"
FT 906..1499
FT /*tag= c
FT /product= E
FT /note= "envelope protein"
FT 1500..2519
FT /*tag= d
FT /product= NS1
FT 2520..3350
FT /*tag= e
FT /product= NS2
FT 3351..5177
FT /*tag= f
FT /product= NS3
FT 5178..5918
FT /*tag= g
FT /product= NS4a
FT 5919..6371
FT /*tag= h
FT /product= NS4b
FT 6372..9365
FT /*tag= i
FT /product= NS5
FT EP-463848-A.
PN 02-JAN-1991.
PD 25-JUN-1991. 305717.
PR 25-JUN-1991; JP-167466.
PR 31-AUG-1990; JP-230921.
PR 09-NOV-1990; JP-305605.
PR 28-DEC-1990; US-635451.
PR 08-MAY-1991; JP-132090.
PR 14-MAY-1991; JP-138493.
PA (OSAU ) Osaka University.
PI Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
DR WPI: 92-009412/02.
DR P-PSDB: R20111.
PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
PT diagnostics and screening agents for NANBV, and to remove NANBV from
PT blood.
PS Disclosure; Fig 2; 89pp; English.
CC The sequence was obtd. from several overlapping "BK" cDNA clones
CC obtd. by "gene walking" using a cDNA clone isolated from a library
CC prepd. from NANBV RNA. The DNA and fragments of it can be used
CC for the detection of the presence of NANBV by hybridisation or PCR.
CC Antigenic polypeptides encoded by the sequence can be used as
CC immunoassay reagents, for screening donated blood, and as immuno-
CC gens for vaccine prodn. Antibodies raised to the peptides can be
CC used in immunoassays to detect or quantify NANBV antigens in liver
CC tissue and blood. Preferred polypeptides are encoded by the
CC following nucleotides: 333-422, -677, or -6371; 474-563; 678-905;
CC 906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
CC 2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5919-
CC 6371; and 6372-9372. The sequence is also disclosed in EP-464287
CC in which it is claimed. See Q21829 for details of this specifi-
CC cation.
CC Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;

Query Match 100.0%; Score 20; DB 1; Length 9416;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgcacggtctacgagacc 20
DB 332 GGTGCACGGTCTACGAGACC 313

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RESULT 9
Q20940/c
ID Q20940 standard; DNA: 807 BP.
AC Q20940;
DT 13-MAY-1992 (first entry)
DE PCR-generated fragment of Hepatitis C virus cDNA from clone M642.
KW Non-A, non-B hepatitis virus; NANBH; ss.
OS Hepatitis C virus.
PN EP-469348-A.
PD 05-FEB-1992.
PF 09-JUL-1991; 111413.
PR 11-JUL-1990; JP-183512.
PR 18-DEC-1990; JP-412177.
PR 30-JAN-1991; JP-029364.
PR 14-FEB-1991; JP-042855.
PA (SHIO ) SHIONOGI KK.
PI Kamada T, Hayashi N, Mita E, Ueda K;
DR WPI: 92-042764/06.
DE cDNA sequence for detection of hepatitis C - isolated from liver
PT of HCV-antibody positive patients for use in polymerase chain
PT reaction
PS Claim 1: Page 23; 26pp; English.
CC RNA was extracted from the liver of a patient with liver cancer.
CC cDNA was prepared from the RNA using an anti-sense primer (see
CC Q20941) and MMuLV reverse transcriptase. The cDNA was amplified by
CC the PCR method using the same anti-sense primer with a sense primer
CC (see Q20942). The PCR product was subjected to a second PCR
CC amplification using a different primer pair (see Q20943 and
CC Q20944). The PCR product was electrophoresed and a single band of
CC the expected size was cut out. DNA was extracted from the gel and
CC cloned in pBluescript II SK(plus). The recombinant vector was used
CC to transform competent E.coli XL-1-B. DNA was extracted from the
CC transformants, digested with BamHI and EcoRI and allowed to migrate
CC on a gel. Positive clones were selected based on the size of the
CC restriction fragments. DNA from one of the positive clones (M642)
CC was sequenced.
CC Sequence 807 BP; 148 A; 253 C; 255 G; 151 T;
SQ

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Query Match 100.0%; Score 20; DB 1; Length 807;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgcacggtctacgagacc 20
DB 325 GGTGCACGGTCTACGAGACC 306

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RESULT 10
Q22871/c
ID Q22871 standard; DNA: 9416 BP.
AC Q22871;
DT 07-JUL-1992 (first entry)
DE NANBV Hutch c59 isolate genome.
KW Hepatitis C virus; non-A non-B virus; HCV-Hc59; primers;
KW probes; vaccine; ss.
OS NANBV Hutch c59 isolate.
FH Key Location/Qualifiers
FT cds 342..9377
FT /*tag= a
FT /label= viral_genome
FT misc_feature 1..12
FT /*tag= b
FT /note= "not confirmed as HCV-Hc59 sequence"
FT misc_feature 9397..9416
FT /*tag= c
FT /note= "not confirmed as HCV-Hc59 sequence"
FT repeat_unit 7..12
FT /*tag= d
FT /rpt_type= 1
FT repeat_unit 42..47
FT /*tag= e

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FT      repeat_unit      /rpt_type= 1
FT      23..28           /tag= f
FT      repeat_unit      /rpt_type= 2
FT      38..43           /tag= g
FT      repeat_unit      /rpt_type= 2
FT      9209..9214       /tag= h
FT      repeat_unit      /rpt_type= 2
FT      9391..9396       /tag= i
FT      repeat_unit      /rpt_type= 2
FT      128..135         /tag= j
FT      repeat_unit      /rpt_type= 3
FT      315..322         /tag= k
FT      repeat_unit      /rpt_type= 3
FT      315..322         /tag= l
FT      repeat_unit      /rpt_type= 3
FT      9231..9237       /tag= m
FT      repeat_unit      /rpt_type= 4
FT      9245..9251       /tag= n
FT      repeat_unit      /rpt_type= 4
FT      9256..9262       /tag= o
FT      repeat_unit      /rpt_type= 4
FT      9248..9253       /tag= p
FT      repeat_unit      /rpt_type= 5
FT      9221..9226       /tag= q
FT      repeat_unit      /rpt_type= 5
FT      9227..9232       /tag= r
FT      misc_difference  /rpt_type= 5
FT      351..353         /tag= s
FT      /label= AAT
FT      /note= "or ATT according to Seq No 1 (Q22838), see CC"
FT      misc_difference  1302..1304
FT      /tag= t
FT      /label= AAT
FT      /note= "or GAT according to Seq No 1 (Q22838), see CC"
FT      misc_rna         /tag= u
FT      /product= NANBV_structural_proteins
FT      342..701
FT      /tag= v
FT      /label= capsid
FT      misc_rna         /tag= w
FT      /label= envelope_protein
FT      1..60
FT      /tag= x
FT      /label=
FT      /note= "pref. capsid antigen"
FT      61..120
FT      /tag= y
FT      /note= "pref. capsid antigen"
FT      4..120
FT      /tag= z
FT      /note= "pref. capsid antigen"
FT      1..222
FT      /tag= aa
FT      /note= "pref. capsid antigen"
FT      205..360
FT      /tag= ab

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FT      misc_feature     /note= "pref. capsid antigen"
FT      361..528
FT      /tag= ac
FT      /note= "pref. envelope antigen"
FT      361..978
FT      /tag= ad
FT      /note= "pref. envelope antigen"
FT      1497..1574
FT      /tag= ae
FT      /label= V_variable_region
FT      1077..1166
FT      /tag= af
FT      /label= V1_variable_region
FT      1707..1787
FT      /tag= ag
FT      /label= V2_variable_region
FT      7407..7478
FT      /tag= ah
FT      /label= V3_variable_region
FT      1512..1553
FT      /tag= ai
FT      /note= "pref. V fragment"
FT      1077..1109
FT      /tag= aj
FT      /note= "pref. V1 fragment"
FT      1722..1739
FT      /tag= ak
FT      /note= "pref. V2 fragment"
FT      1758..1787
FT      /tag= al
FT      /note= "pref. V2 fragment"
FT      488..504
FT      /tag= am
FT      /label= oligonucleotide_693
FT      /note= "used in NANBV cloning"
FT      complement (549..565)
FT      /tag= an
FT      /label= oligonucleotide_694
FT      /note= "used in NANBV cloning"
FT      complement (681..701)
FT      /tag= ao
FT      /label= oligonucleotide_691
FT      /note= "used in NANBV cloning"
FT      697..715
FT      /tag= ap
FT      /label= oligonucleotide_14
FT      /note= "used in NANBV cloning"
FT      702..718
FT      /tag= aq
FT      /label= oligonucleotide_15
FT      /note= "used in NANBV cloning"
FT      complement (853..870)
FT      /tag= ar
FT      /label= oligonucleotide_18
FT      /note= "used in NANBV cloning"
FT      WO9203458-A.
FT      05-MAR-1992.      U06037.
FT      23-AUG-1991;     PF
FT      25-AUG-1990;     PR
FT      21-NOV-1990;     US-616369.
FT      (NYBL-) NEW YORK BLOO DCENT.
FT      (PHAA) PHARMACIA GENETIC ENG INC.
FT      Zebedee S, Inchauspe G, Nasofe MS, Prince AM;
FT      WPI: 92-096821/12.
FT      P-PSDB: R22154.
FT      Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis
FT      virus - Obtd. Hutch C59 subgroup encoding polypeptide(s), useful
FT      as vaccines, and immuno reactive Abs for diagnosis of virus
FT      disclosure; Page 159-173; 225pp; English.
FT      One Hutch strain (HCV-H) of NANBV, designated the Hutch c59 isolate
FT      (HCV-Hc59) was propagated through passage in animals and the
FT      entire viral genome was cloned and sequenced.
FT      The sequence in Q22838 (tag u) comprises two bases, indicated in

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CC the features, which differ from the sequence represented here.
 CC Two more oligonucleotides used in NANBV cloning are shown in
 CC Q22838, and one in Q22859.
 CC The encoded proteins and peptides (see features) and antibodies
 CC against them are useful for the prep. of vaccines and inoculums
 CC against NANBV and in immunological assays for detection of viral
 CC infection. The nucleic acid may be used to detect the presence of
 CC NANBV DNA.
 CC Nucleotide sequences used in the prodn. of polynucleotides are
 CC selected from the V, VI, V2 and V3 variable region. The regions
 CC indicated in the features encode peptides contg. the greatest amt. of
 CC diversity when compared to known HCV isolates. The polynucleotides
 CC may be used as primers, probes, or a nucleic acids.
 SQ Sequence 9416 BP; 1879 A; 2849 C; 2683 G; 2005 T;

Query Match 100.0%; Score 20; DB 1; Length 9416;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtgcacgggtctacgagacc 20
 |||||
 Db 341 GGTGCACGGTCTACGAGACC 322

RESULT 11
 Q24467/c
 ID Q24467 standard; DNA; 1880 BP.
 AC Q24467;
 DT 09-NOV-1992 (first entry)
 DE NANB hepatitis virus strain HC-J4 genome.
 KW non-A, non-B hepatitis virus; NANBH; PCR; amplification
 KW polymerase chain reaction; vaccine; antibody; ss.
 OS Non-A, non-B hepatitis virus.
 FH Key Location/Qualifiers
 FT 342..1880
 FT /*tag= a
 FT /label= HC-J4
 PN EP-485209-A.
 PD 13-MAY-1992.
 PF 07-NOV-1991; 310297.
 PR 08-NOV-1990; JP-304405.
 PA (IMMO) IMMUNO JAPAN INC.
 PI Nakamura T, Okamoto H;
 DR WPI; 92-160959/20.
 DR P-PSDB; R24087.
 PT Recombinant cDNA of NANBV virus strain HC-J5 and corresp.
 PT peptides - useful for diagnosis and in vaccines and immunological
 PT pharmaceuticals
 PS Disclosure: Page 11; 42pp; English.
 CC This sequence is the genome of the non-A, non-B hepatitis virus
 CC (NANBH) strain HC-J4. This sequence was derived by amplification
 CC by polymerase chain reaction. The nucleotide sequences derived from
 CC this amplification can be used to detect NANBH infection which could
 CC not be detected by conventional methods. The detection kits allow
 CC highly specific and sensitive detection at an early phase of
 CC infection. The polypeptide product of this coding sequence can be used
 CC for the manufacture of vaccines and immunological pharmaceuticals
 CC and also to produce antibodies specific to NANBH.
 SQ Sequence 1880 BP; 333 A; 593 C; 556 G; 398 T;

Query Match 100.0%; Score 20; DB 1; Length 1880;
 Best Local Similarity 100.0%; Pred. No. 0.072;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtgcacgggtctacgagacc 20
 |||||
 Db 341 GGTGCACGGTCTACGAGACC 322

RESULT 12
 Q24468/c
 ID Q24468 standard; DNA; 1886 BP.
 AC Q24468;
 DT 09-NOV-1992 (first entry)
 DE NANB hepatitis virus strain HC-J5 genome.
 KW non-A, non-B hepatitis virus; NANBH; PCR; amplification
 KW polymerase chain reaction; vaccine; antibody; ss.
 OS Non-A, non-B hepatitis virus.
 FH Key Location/Qualifiers
 FT 342..1886
 FT /*tag= a
 FT /label= HC-J5
 PN EP-485209-A.
 PD 13-MAY-1992.
 PF 07-NOV-1991; 310297.
 PR 08-NOV-1990; JP-304405.
 PA (IMMO) IMMUNO JAPAN INC.
 PI Nakamura T, Okamoto H;
 DR WPI; 92-160959/20.
 DR P-PSDB; R24088.
 PT Recombinant cDNA of NANBV virus strain HC-J5 and corresp.
 PT peptides - useful for diagnosis and in vaccines and immunological
 PT pharmaceuticals
 PS Disclosure: Page 8; 42pp; English.
 CC This sequence is the genome of the non-A, non-B hepatitis virus
 CC (NANBH) strain HC-J5. This sequence was derived by amplification
 CC by polymerase chain reaction. The nucleotide sequences derived from
 CC this amplification can be used to detect NANBH infection which could
 CC not be detected by conventional methods. The detection kits allow
 CC highly specific and sensitive detection at an early phase of
 CC infection. The polypeptide product of this coding sequence can be used
 CC for the manufacture of vaccines and immunological pharmaceuticals
 CC and also to produce antibodies specific to NANBH.
 SQ Sequence 1886 BP; 365 A; 582 C; 542 G; 397 T;

Query Match 100.0%; Score 20; DB 1; Length 1886;
 Best Local Similarity 100.0%; Pred. No. 0.072;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtgcacgggtctacgagacc 20
 |||||
 Db 341 GGTGCACGGTCTACGAGACC 322

RESULT 13
 Q24466/c
 ID Q24466 standard; DNA; 1880 BP.
 AC Q24466;
 DT 09-NOV-1992 (first entry)
 DE NANB hepatitis virus strain HC-J1 genome.
 KW non-A, non-B hepatitis virus; NANBH; PCR; amplification
 KW polymerase chain reaction; vaccine; antibody; ss.
 OS Non-A, non-B hepatitis virus.
 FH Key Location/Qualifiers
 FT 342..1880
 FT /*tag= a
 FT /label= HC-J1
 PN EP-485209-A.
 PD 13-MAY-1992.
 PF 07-NOV-1991; 310297.
 PR 08-NOV-1990; JP-304405.
 PA (IMMO) IMMUNO JAPAN INC.
 PI Nakamura T, Okamoto H;
 DR WPI; 92-160959/20.
 DR P-PSDB; R24086.
 PT Recombinant cDNA of NANBV virus strain HC-J5 and corresp.
 PT peptides - useful for diagnosis and in vaccines and immunological
 PT pharmaceuticals
 PS Disclosure: Page 8; 42pp; English.
 CC This sequence is the genome of the non-A, non-B hepatitis virus
 CC (NANBH) strain HC-J1. This sequence was derived by amplification
 CC by polymerase chain reaction. The nucleotide sequences derived from
 CC this amplification can be used to detect NANBH infection which could

CC not be detected by conventional methods. The detection kits allow
 CC highly specific and sensitive detection at an early phase of
 CC infection. The polypeptide product of this coding sequence can be used
 CC for the manufacture of vaccines and immunological pharmaceuticals
 CC and also to produce antibodies specific to NANBHV.
 SQ Sequence 1880 BP; 349 A; 582 C; 546 G; 403 T;

Query Match 100.0%; Score 20; DB 1; Length 1880;
 Best Local Similarity 100.0%; Pred. No. 0.072;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgcacgggtctacgagacc 20
 |||||
 Db 341 GGTGCACGGTCTACGAGACC 322

RESULT 14

Q27159/c
 ID Q27159 standard; cDNA; 1682 BP.
 AC Q27159;
 DT 27-JAN-1993 (first entry)
 DE NANB hepatitis virus DNA clone.
 KW Non-A; Non-B; NANBH; vaccine; ss.
 OS Non-A; Non-B Hepatitis virus.
 PN J04187090-A.
 PD 03-JUL-1992.
 PF 22-NOV-1990; 319195.
 PR 22-NOV-1990; JP-319195.
 PA (GREC) GREEN CROSS CORP.
 PA (SHIK/) SHIKATA T.
 DR WPI: 92-273647/33.
 DR N-PSDB; R25989.
 PT Non-A, non-B hepatitis antigen and DNA encoding it - is useful in
 PT diagnosing NANBH and as a vaccine
 PS Page 8; Fig 1; 10pp; Japanese.
 CC The cDNA sequence was obtd. by screening a NANB hepatitis cDNA
 CC library in lambda gt11 with probe obtd. by primary screen of a
 CC NANB hepatitis library of inserts in lambda gt10 (see Q27158).
 CC Probe hybridisation gave rise to two clones for NANB hepatitis
 CC virus DNA, both of which were subcloned into pUC18 and sequenced
 CC (the sequence of one cloned showed here). The polypeptides encoded
 CC by these clones are useful in the diagnosis of NANB hepatitis virus
 CC and in commercial prodn. of a virus against NANB hepatitis virus.
 CC See also Q27158-61 and Q33031.
 SQ Sequence 1682 BP; 311 A; 505 C; 488 G; 378 T;

Query Match 100.0%; Score 20; DB 1; Length 1682;
 Best Local Similarity 100.0%; Pred. No. 0.072;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgcacgggtctacgagacc 20
 |||||
 Db 24 GGTGCACGGTCTACGAGACC 5

RESULT 15

Q27697/c
 ID Q27697 standard; RNA; 117 BP.
 AC Q27697;
 DT 29-JAN-1993 (first entry)
 DE Oligomer GBI corresp. to RNA for an epitope of HCV.
 KW Hepatitis C virus; probe; antibodies; liver; replication; ds.
 OS Synthetic.
 PN W09212992-A.
 PD 06-AUG-1992.
 PF 14-JAN-1992; U00356.
 PR 14-JAN-1991; US-639809.
 PA (GAMB-) GAMBLE INST MEDICAL RES JAMES N.
 PI Baroudy BM, Kotwal GJ;
 DR WPI: 92-284597/34.
 PT Basic structural immunogenic peptide(s) having epitope(s) for HCV

PT - useful as vaccines against HCV infection; also for diagnosis of
 PT HCV and auto-immune liver disease
 PS Claim 85; Page 119; 244pp; English.
 CC The ds DNA fragment may be synthesised and when ligated in frame
 CC into appropriate vectors an introduced into infected liver cells is
 CC able to transcribe the antisense polynucleotide RNA of FGB1.
 CC The synthetic antisense RNA sequence can block protein translation
 CC and/or HCV RNA replication by specifically binding to their target
 CC sequence. Thus the antisense oligonucleotide may be used for
 CC treatment of HCV. See also Q27675-96.
 SQ Sequence 117 BP; 32 A; 38 C; 30 G; 17 T;

Query Match 100.0%; Score 20; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.062;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggtgcacgggtctacgagacc 20
 |||||
 Db 33 GGTGCACGGTCTACGAGACC 14

Search completed: November 23, 1999, 13:58:53
 Job time: 6680 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 23, 1999, 13:58:53 ; Search time 70.49 Seconds
(without alignments)
70.987 Million cell updates/sec

Title: US-09-031-087-3
Perfect score: 20
Sequence: 1 ccggagagaccatagtgttc 20

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20	100.0	9185	1	Q05956
2	20	100.0	9185	1	Q10566
3	20	100.0	504	1	Q12239
4	20	100.0	2116	1	Q12242
5	20	100.0	202	1	Q14083
6	20	100.0	202	1	HCV-T (1-202). New
7	20	100.0	202	1	HCV-KU (1-202). Ne
8	20	100.0	202	1	HCV-N (1-200). New
9	20	100.0	202	1	HCV-I (1-202). New
10	20	100.0	1863	1	Q15363
11	20	100.0	1863	1	Q15362
12	20	100.0	9416	1	Q21829
13	20	100.0	9416	1	Q20268
14	20	100.0	9400	1	Q21744
15	20	100.0	9416	1	Q22871
16	20	100.0	1880	1	Q24467
17	20	100.0	1886	1	Q24468
18	20	100.0	1880	1	Q24466
19	20	100.0	2540	1	Q29628
20	20	100.0	1885	1	Q29629
21	20	100.0	2551	1	Q29630
22	20	100.0	2498	1	Q29631
23	20	100.0	252	1	Q31071
24	20	100.0	252	1	Q31072
25	20	100.0	252	1	Q31078
26	20	100.0	252	1	Q31079
27	20	100.0	252	1	Q31066
28	20	100.0	252	1	Q31067
29	20	100.0	252	1	Q31068
30	20	100.0	252	1	Q31069
31	20	100.0	252	1	Q31070
32	20	100.0	252	1	Q31080
33	20	100.0	252	1	Q31081
34	20	100.0	180	1	Q31082
35	20	100.0	180	1	Q31083
36	20	100.0	483	1	Q32444
37	20	100.0	483	1	Q32445
38	20	100.0	483	1	Q32446
39	20	100.0	483	1	Q32447
40	20	100.0	1554	1	Q32451
41	20	100.0	483	1	Q32453
42	20	100.0	256	1	Q32981
43	20	100.0	9472	1	Q33282

ALIGNMENTS

RESULT 1

Q05956
ID Q05956 standard; DNA; 9185 BP.
AC Q05956;
DT 23-JAN-1991 (first entry)
DE Sense strand of the compiled Hepatitis C virus cDNA sequence.
KW Hepatitis C virus (HCV); antiviral agent; ss.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT cds 320..9185
FT misc_rna 1..1667
FT /*tag= a
FT /*tag= b
FT /*note="epitope within this region is claimed"
FT misc_rna 8978..9185
FT /*tag= c
FT /*note="encodes an epitope that is claimed"
PN EP-388232-A.
PD 19-SEP-1990.
PF 16-MAR-1990; 302866.
PR 17-MAR-1989; US-325338.
PR 20-APR-1989; US-341334.
PR 18-MAY-1989; US-355002.
PR (CHIR-) CHIRON CORP.
PA Houghton M, Choo QL, Kuo G.;
PI WPI: 90-284418/38.
DR P-PSDB; R08124.
PT Hepatitis C virus DNA - used for producing probes,
polyptide(s), antibodies and anti-sense polynucleotide(s) for
diagnosis and therapy.
PS Disclosure: Fig 17; 83pp; English.
CC HCV cDNA libraries were constructed using pooled serum from a
chimpanzee with chronic HCV infection. A lambda gt11 library was
screened with probes derived from previously isolated clones. The
ORF is derived from the overlapping clones b14a, ag30a, CA205a,
CA290a, CA216a, p14a, CA167b, CA156e, CA84a, CA59a, K9-1, 26j, 13i,
12f, 14i, 11b, 7f, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c,
14c, 8f, 33f, 33g, 39c, 35f, 19g, 26g, 15e, b5a and 16jh. These
clones extend the sequence of the HCV genome reported in EP-318216.
CC The upstream region from nucleotides -319 to +1348 (-1-1667 in this
file) is covered by clones b14a, 18g, ag30a, CA205a, CA290a,
CA216a, p14a, CA167b, CA156e, CA84a and CA59a; nucleotides
8659-8866 (=8978-9185 in this file) are covered by clones b5a and
16jh.
CC See also Q05955.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;

Query Match 100.0%; Score 20; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccggagagaccatagtgttc 20
|||||
DB 107 CCGGGAGAGCCATAGTGGTC 126

RESULT 2

Q10566
ID Q10566 standard; DNA; 9185 BP.
AC Q10566;
DT 29-APR-1991 (first entry)
DE Hepatitis C virus strain 1 DNA.
KW Hepatitis C virus; HCV-1; non-A, non-B hepatitis; HCV antigen;
viral infections; ss.
OS Hepatitis C virus.

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PN EP-414475-A.
PD 27-FEB-1991.
PF 21-AUG-1990; 309120.
PR 25-AUG-1989; US-398667.
PA (CHIR-) CHIRON CORP.
PI Weiner AJ, Steimer KS;
DR WPI; 91-059670/03.
PT Cell lines infected with hepatitis C virus - are used as source
PT of antigens for detection of HCV antibodies, for vaccines, and
PT for screening anti-viral agents
PS Disclosure; fig 1; 24pp; English.
CC This is a hepatitis C virus (HCV) composite cDNA sequence, deduced
CC using overlapping clones. a compsn. contg. the antigenic protein
CC bodies (Abs) and for screening an agent which inhibits HCV replic-
CC ation. A cell line infected with this virus can be used as a
CC source of antigens. The antigen is useful for preparing vaccines
CC for treating viral infections. See also Q10567.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;

Query Match 100.0%; Score 20; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtgttc 20
   |||||||
Db 107 CCGGAGAGCCATAGTGTC 126

RESULT 3
Q12239
ID Q12239 standard; DNA; 504 BP.
AC Q12239;
DT 06-SEP-1991 (first entry)
DE Clone 164/137 encoding PT-NANBH virus antigenic portion.
KW post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 308..504
FT /*tag= a
FT /product= start of PT-NANBH polyprotein
PN GB2239245-A.
PD 26-JUN-1991.
PF 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI; 91-187584/26.
DR P-PSDB; R12597.
PT Post-transfusional non-A non-B hepatitis poly:peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 71-72; 108pp; English.
CC This sequence probably encodes viral structural proteins of the
CC PT-NANBH viral genome having antigenic properties. It was
CC isolated from serum of humans infected by the virus.
CC See also Q12236-8 and Q12240-Q1242.
SQ Sequence 504 BP; 106 A; 147 C; 153 G; 98 T;

Query Match 100.0%; Score 20; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtgttc 20
   |||||||
Db 95 CCGGAGAGCCATAGTGTC 114

RESULT 4
Q12239
ID Q12239 standard; DNA; 504 BP.
AC Q12239;
DT 06-SEP-1991 (first entry)
DE Clone 164/137 encoding PT-NANBH virus antigenic portion.
KW post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 308..504
FT /*tag= a
FT /product= start of PT-NANBH polyprotein
PN GB2239245-A.
PD 26-JUN-1991.
PF 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI; 91-187584/26.
DR P-PSDB; R12597.
PT Post-transfusional non-A non-B hepatitis poly:peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 71-72; 108pp; English.
CC This sequence probably encodes viral structural proteins of the
CC PT-NANBH viral genome having antigenic properties. It was
CC isolated from serum of humans infected by the virus.
CC See also Q12236-8 and Q12240-Q1242.
SQ Sequence 504 BP; 106 A; 147 C; 153 G; 98 T;

Query Match 100.0%; Score 20; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtgttc 20
   |||||||
Db 95 CCGGAGAGCCATAGTGTC 114

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Q12242
ID Q12242 standard; DNA; 2116 BP.
AC Q12242;
DT 17-SEP-1991 (first entry)
DE Encodes PT-NANBH viral structural and non-structural proteins.
KW post-transfusional non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 308..2116
FT /*tag= a
FT /product= start of PT-NANBH polyprotein
PN GB2239245-A.
PD 26-JUN-1991.
PF 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI; 91-187584/26.
DR P-PSDB; R12600.
PT Post-transfusional non-A non-B hepatitis poly:peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 83-87; 108pp; English.
CC This sequence is thought to encode viral structural and non-
CC structural proteins of the PT-NANBH viral genome which are antigenic.
CC It was isolated from human serum infectious for the virus.
CC See also Q12236-41.
SQ Sequence 2116 BP; 392 A; 650 C; 624 G; 450 T;

Query Match 100.0%; Score 20; DB 1; Length 2116;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtgttc 20
   |||||||
Db 95 CCGGAGAGCCATAGTGTC 114

RESULT 5
Q14083
ID Q14083 standard; DNA; 202 BP.
AC Q14083;
DT 03-JAN-1992 (first entry)
DE HCV-T (1-202).
KW Epitope; PCR; diagnosis; ss.
OS Hepatitis C virus.
PN W09114779-A.
PD 03-OCT-1991.
PF 28-MAR-1991; J00405.
PF 28-MAR-1990; JP-080185.
PR 13-JUN-1990; JP-154230.
PR 14-JUN-1990; JP-153979.
PR 03-NOV-1990; JP-305795.
PA (MITK) MITSUI TOATSU CHEM INC.
PI Takada T, Enomoto N, Date T, Nakao T;
DR WPI; 91-310579/42.
PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
PT of hepatitis C virus infection via polymerase chain reaction
PS Disclosure; Fig 1(i); 79pp; Japanese.
CC The nucleotide sequences represented in Q14076-86 and Q14767-71
CC encode epitopes from structural, non-structural and 5' untranslated
CC domains of hepatitis C virus. The sequences are used for accurate
CC and simple diagnosis and typing of HCV infection, using PCR
CC amplification techniques.
SQ Sequence 202 BP; 39 A; 61 C; 61 G; 41 T;

Query Match 100.0%; Score 20; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 ccgggagagccatagtgttc 20
 |||||
 Db 86 CCGGAGAGCCATAGTGTC 105

RESULT 6

Q14085
 ID Q14085 standard; DNA; 202 BP.
 AC Q14085;
 DT 03-JAN-1992 (first entry)
 DE HCV-KU (1-202).
 KW Epitope; PCR; diagnosis; ss.
 OS Hepatitis C virus.
 PN WO9114779-A.
 PD 03-OCT-1991.
 PF 28-MAR-1991; J00405.
 PR 28-MAR-1990; JP-080185.
 PR 13-JUN-1990; JP-154230.
 PR 14-JUN-1990; JP-153979.
 PR 09-NOV-1990; JP-305795.
 PA (MITK) MITSUI TOATSU CHEM INC.
 PI Takada T, Enomoto N, Date T, Nakao T;
 DR WPI; 91-310579/42.
 PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
 of hepatitis C virus infection via polymerase chain reaction
 PS Disclosure; Fig 1(I); 79pp; Japanese.
 CC The nucleotide sequences represented in Q14076-86 and Q14767-71
 encode epitopes from structural, non-structural and 5' untranslated
 domains of hepatitis C virus. The sequences are used for accurate
 and simple diagnosis and typing of HCV infection, using PCR
 amplification techniques.
 CC amplification techniques.
 SQ Sequence 202 BP; 40 A; 61 C; 58 G; 43 T;

Query Match 100.0%; Score 20; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtgttc 20
 |||||
 Db 86 CCGGAGAGCCATAGTGTC 105

RESULT 7

Q14086
 ID Q14086 standard; DNA; 202 BP.
 AC Q14086;
 DT 03-JAN-1992 (first entry)
 DE HCV-N (1-200).
 KW Epitope; PCR; diagnosis; ss.
 OS Hepatitis C virus.
 PN WO9114779-A.
 PD 03-OCT-1991.
 PF 28-MAR-1991; J00405.
 PR 28-MAR-1990; JP-080185.
 PR 13-JUN-1990; JP-154230.
 PR 14-JUN-1990; JP-153979.
 PR 09-NOV-1990; JP-305795.
 PA (MITK) MITSUI TOATSU CHEM INC.
 PI Takada T, Enomoto N, Date T, Nakao T;
 DR WPI; 91-310579/42.
 PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
 of hepatitis C virus infection via polymerase chain reaction
 PS Disclosure; Fig 1(I); 79pp; Japanese.
 CC The nucleotide sequences represented in Q14076-86 and Q14767-71
 encode epitopes from structural, non-structural and 5' untranslated
 domains of hepatitis C virus. The sequences are used for accurate
 and simple diagnosis and typing of HCV infection, using PCR
 amplification techniques.
 CC amplification techniques.
 SQ Sequence 202 BP; 42 A; 60 C; 56 G; 44 T;

Query Match 100.0%; Score 20; DB 1; Length 202;

Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtgttc 20
 |||||
 Db 86 CCGGAGAGCCATAGTGTC 105

RESULT 8

Q14084
 ID Q14084 standard; DNA; 202 BP.
 AC Q14084;
 DT 03-JAN-1992 (first entry)
 DE HCV-I (1-202).
 KW Epitope; PCR; diagnosis; ss.
 OS Hepatitis C virus.
 PN WO9114779-A.
 PD 03-OCT-1991.
 PF 28-MAR-1991; J00405.
 PR 28-MAR-1990; JP-080185.
 PR 13-JUN-1990; JP-154230.
 PR 14-JUN-1990; JP-153979.
 PR 09-NOV-1990; JP-305795.
 PA (MITK) MITSUI TOATSU CHEM INC.
 PI Takada T, Enomoto N, Date T, Nakao T;
 DR WPI; 91-310579/42.
 PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
 of hepatitis C virus infection via polymerase chain reaction
 PS Disclosure; Fig 1(I); 79pp; Japanese.
 CC The nucleotide sequences represented in Q14076-86 and Q14767-71
 encode epitopes from structural, non-structural and 5' untranslated
 domains of hepatitis C virus. The sequences are used for accurate
 and simple diagnosis and typing of HCV infection, using PCR
 amplification techniques.
 CC amplification techniques.
 SQ Sequence 202 BP; 41 A; 60 C; 60 G; 41 T;

Query Match 100.0%; Score 20; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtgttc 20
 |||||
 Db 86 CCGGAGAGCCATAGTGTC 105

RESULT 9

Q15363
 ID Q15363 standard; DNA; 1863 BP.
 AC Q15363;
 DT 17-MAR-1992 (first entry)
 DE Fragment of NANB hepatitis virus strain HC-J4.
 KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
 OS polymerase chain reaction; ss.
 OS Hepatitis C virus.
 FH Key Location/Qualifiers
 FT 5'utr 1..324
 FT cds 325..1863
 FT /*tag= a
 FT /*tag= b
 PN EP-461863-A.
 DR 18-DEC-1991.
 PF 11-JUN-1991; 305270.
 PR 12-JUN-1990; JP-153402.
 PA (IMMU-) IMMUNO JAPAN INC.
 PI Okamoto H, Ogikubo Y;
 DR WPI; 91-370834/51.
 PT Oligo-nucleotide primers - derived from and used to detect and
 diagnose non-A, non-B hepatitis virus
 PS Claim 1; Page 7; 23pp; English.
 CC NANB hepatitis virus strain HC-J4 was isolated from a plasma sample
 of a chimpanzee challenged with NANB hepatitis for infectivity but
 which tested negative for HCV antibody by Ortho HCV Ab ELISA test.

CC RNA was isolated from the sample and reverse transcribed into cDNA.
 CC The 513 amino acids encoded by the CDS were determined but are not
 CC given in the specification (and hence are not included in A-Geneseq).
 CC A study of the deduced sequence suggested that the CDS encodes NANBH
 CC virus core proteins. Primers for detecting NANBH hepatitis virus were
 CC designed based on the HC-J4 sequence.
 SQ Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T;

Query Match 100.0%; Score 20; DB 1; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtggc 20
 |||||
 Db 112 CCGGGAGAGCCATAGTGGTC 131

RESULT 10
 ID Q15362 standard; cDNA; 1863 BP.
 AC Q15362;
 DT 17-MAR-1992 (first entry)
 DE Fragment of NANBH hepatitis virus strain HC-J1.
 KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
 KW polymerase chain reaction; ss.
 OS Hepatitis C virus.
 FH Key Location/Qualifiers
 FT 5'utr 1..324
 FT /tag= a
 FT cds 325..1863
 FT /tag= b

FT EP-461863-A.
 PN 18-DEC-1991.
 PD 11-JUN-1991; 305270.
 PF 12-JUN-1990; JP-153402.
 PR (IMMU-) IMMUNO JAPAN INC.
 PA Okamoto H, Ogikubo Y;
 PI WPI; 91-370834/51.
 DR Oligo-nucleotide primers - derived from and used to detect and
 PT diagnose non-A, non-B hepatitis virus
 PS Claim 1; Page 7; 23pp; English.
 CC NANBH hepatitis virus strain HC-J1 was isolated from a plasma sample
 CC of a Japanese blood donor who tested positive for HCV antibody. RNA
 CC was isolated from the sample and reverse transcribed into cDNA. The
 CC 513 amino acids encoded by the CDS were determined but are not given
 CC in the specification (and hence are not included in A-Geneseq). A
 CC study of the deduced sequence suggested that the CDS encodes NANBH
 CC virus core proteins. Primers for detecting NANBH hepatitis virus were
 CC designed based on the HC-J1 sequence.
 SQ Sequence 1863 BP; 347 A; 581 C; 533 G; 402 T;

Query Match 100.0%; Score 20; DB 1; Length 1863;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtggc 20
 |||||
 Db 112 CCGGGAGAGCCATAGTGGTC 131

RESULT 11
 ID Q21829 standard; cDNA; 9416 BP.
 AC Q21829;
 DT 01-MAY-1997 (first entry)
 DE Non-A, non-B viral genome.
 KW NANBH; vaccine; immunodiagnosis; antigen; antibody; ds.
 OS Non-A, non-B hepatitis virus.
 FH Key Location/Qualifiers
 FT 333..677
 FT cds /tag= a

FT /product= C
 FT /note= "core protein"
 FT 678..905
 FT /tag= b
 FT /product= M
 FT /note= "matrix protein"
 FT 906..1499
 FT /tag= c
 FT /product= E
 FT /note= "envelope protein"
 FT 1500..2519
 FT /tag= d
 FT /product= NS1
 FT 2520..3350
 FT /tag= e
 FT /product= NS2
 FT 3351..5177
 FT /tag= f
 FT /product= NS3
 FT 5178..5918
 FT /tag= g
 FT /product= NS4a
 FT 5919..6371
 FT /tag= h
 FT /product= NS4b
 FT 6372..9365
 FT /tag= i
 FT /product= NS5
 PN EP-464287-A.
 PD 08-JAN-1992.
 PF 28-DEC-1990; 314371.
 PR 25-JUN-1990; JP-167466.
 PR 31-AUG-1990; JP-230921.
 PR 09-NOV-1990; JP-305605.
 PA (OSAU) Osaka University.
 PI Okayama H, Fuke I, Morii C, Takamizawa A, Yoshida I;
 DR WPI; 92-009617/02.
 DR P-PSDB; R20091.
 PT Non-A, non-B hepatitis virus (NANBH) particles - as vaccine, immuno-
 PT diagnostics and screening agents for NANBV, and to remove NANBV from
 PS blood.
 PS Claim 1; Fig 2; 89pp; English.
 CC The sequence was obtd. from several overlapping "BK" cDNA clones
 CC obtd. by "gene walking" using a cDNA clone isolated from a library
 CC prep. from NANBV RNA. The DNA and fragments of it can be used
 CC for the detection of the presence of NANBV by hybridisation or PCR.
 CC Antigenic polypeptides encoded by the sequence can be used as
 CC immunoassay reagents, for screening donated blood, and as immuno-
 CC gens for vaccine prodn. Antibodies raised to the peptides can be
 CC used in immunoassays to detect or quantify NANBV antigens in liver
 CC tissue and blood. Preferred polypeptides are encoded by the
 CC following nucleotides: 333-422, -677, or -6371; 474-563; 678-905;
 CC 906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
 CC 2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5919-
 CC 6371; and 6372-9372. The sequence is also disclosed in EP-463848
 CC in which a virus particle contg. antigens encoded by the sequence
 CC is claimed, as well as expression vectors contg. the sequence.
 CC See Q20268 for details of this specification.
 SQ Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;

Query Match 100.0%; Score 20; DB 1; Length 9416;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccgggagagccatagtggc 20
 |||||
 Db 120 CCGGGAGAGCCATAGTGGTC 139

RESULT 12
 Q20268
 ID Q20268 standard; cDNA; 9416 BP.

PI Kolberg JA;
 DR WPI: 92-080094/10.
 DR P-PSDB: R21519.
 DR Reagents for isolating, amplifying and detecting HCV
 PT polynucleotide(s) - used to monitor spread of blood-borne non-A,
 PT non-B hepatitis virus infection and screen blood samples for
 PT virus
 PS Disclosure: Fig 1; 67pp; English.
 CC The sequence is a composite of HCV cDNA from HCV1, a prototypic
 CC HCV. The sequence is based upon sequence information derived from
 CC a no. of HCV cDNA clones, which were isolated from a no. of HCV
 CC cDNA libraries, including the "c" library present in lambda gt11
 CC (ATCC No. 40394), and from human serum. The HCV cDNA clones
 CC were isolated by methods described in W9014436.
 CC The clones from which the sequence was derived are 5'clone32,
 CC b114a, 18g, ag30a, CA205a, CA290a, CA216a, p114a, CA167b, CA156e,
 CC CA84a, CA59a, K9-1 (also called K9-1), 26j, 13i, 12f, 14i, 11b, 7f,
 CC 7e, 8h, 33c, 40b, 37b, 35, 36, 8i, 32, 33b, 25c, 14c, 8f, 33g, 33g,
 CC 39c, 35f, 19g, 26g, 15e, b5a, 16jh, 6k and p131jh.
 CC The target regions indicated in the features are listed in claim 1,
 CC page 49. Oligomers are provided which are complementary to these
 CC target regions and used in the detection of an HCV sequence in an
 CC analyte.
 SQ Sequence 9400 BP; 1885 A; 2860 C; 2671 G; 1984 T;

Query Match 100.0%; Score 20; DB 1; Length 9400;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccggagagaccatagtgtc 20
 |||||
 Db 129 CCGGAGAGCCATAGTGTGTC 148

RESULT 14

Q22871
 ID Q22871 standard; DNA; 9416 BP.
 AC Q22871; 1992 (first entry)
 DE NABV Hutch c59 isolate genome.
 KW Hepatitis C virus: non-A non-B virus; HCV-Hc59; primers;
 OS probes: vaccine; ss.
 KW NABV Hutch c59 isolate.
 FH Key Location/Qualifiers
 FT cds 342..9377
 FT /*tag= a
 FT /label= viral_genome
 FT misc_feature 1..12
 FT /*tag= b
 FT /note= "not confirmed as HCV-Hc59 sequence"
 FT misc_feature 9397..9416
 FT /*tag= c
 FT /note= "not confirmed as HCV-Hc59 sequence"
 FT repeat_unit 7..12
 FT /*tag= d
 FT /rpt_type= 1
 FT repeat_unit 42..47
 FT /*tag= e
 FT /rpt_type= 1
 FT repeat_unit 23..28
 FT /*tag= f
 FT /rpt_type= 2
 FT repeat_unit 38..43
 FT /*tag= g
 FT /rpt_type= 2
 FT repeat_unit 9209..9214
 FT /*tag= h
 FT /rpt_type= 2
 FT repeat_unit 9391..9396
 FT /*tag= i
 FT /rpt_type= 2
 FT repeat_unit 128..135

FT /*tag= j
 FT /rpt_type= 3
 FT repeat_unit 315..322
 FT /*tag= k
 FT /rpt_type= 3
 FT repeat_unit 315..322
 FT /*tag= l
 FT /rpt_type= 3
 FT repeat_unit 9231..9237
 FT /*tag= m
 FT /rpt_type= 4
 FT repeat_unit 9245..9251
 FT /*tag= n
 FT /rpt_type= 4
 FT repeat_unit 9256..9262
 FT /*tag= o
 FT /rpt_type= 4
 FT repeat_unit 9248..9253
 FT /*tag= p
 FT /rpt_type= 5
 FT repeat_unit 9221..9226
 FT /*tag= q
 FT /rpt_type= 5
 FT repeat_unit 9227..9232
 FT /*tag= r
 FT /rpt_type= 5
 FT misc_difference 351..353
 FT /*tag= s
 FT /label= AAT
 FT /note= "or ATT according to Seq No 1 (Q22838), see CC"
 FT misc_difference 1302..1304
 FT /*tag= t
 FT /label= AAT
 FT /note= "or GAT according to Seq No 1 (Q22838), see CC"
 FT misc_rna 342..1319
 FT /*tag= u
 FT /product= NABV_structural_proteins
 FT /note= "Seq No 1 (Q22838)"
 FT misc_rna 342..701
 FT /*tag= v
 FT /label= capsid
 FT misc_rna 702..1319
 FT /*tag= w
 FT /label= envelope_protein
 FT misc_feature 1..60
 FT /*tag= x
 FT /label= x
 FT /note= "pref. capsid antigen"
 FT misc_feature 61..120
 FT /*tag= y
 FT /note= "pref. capsid antigen"
 FT misc_feature 4..120
 FT /*tag= z
 FT /note= "pref. capsid antigen"
 FT misc_feature 1..222
 FT /*tag= aa
 FT /note= "pref. capsid antigen"
 FT misc_feature 205..360
 FT /*tag= ab
 FT /note= "pref. capsid antigen"
 FT misc_feature 361..528
 FT /*tag= ac
 FT /note= "pref. envelope antigen"
 FT misc_feature 361..978
 FT /*tag= ad
 FT /note= "pref. envelope antigen"
 FT misc_feature 1497..1574
 FT /*tag= ae
 FT /label= V_variable_region
 FT misc_feature 1077..1166
 FT /*tag= af
 FT /label= V1_variable_region
 FT misc_feature 1707..1787

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FT FT      /*tag= ag
FT FT      /label= v2_variable_region
FT FT      7407..7478
FT FT      /*tag= an
FT FT      /label= v3_variable_region
FT FT      1512..1553
FT FT      /*tag= ai
FT FT      /note= "pref. V fragment"
FT FT      1077..1109
FT FT      /*tag= aj
FT FT      /note= "pref. V1 fragment"
FT FT      1722..1739
FT FT      /*tag= ak
FT FT      /note= "pref. V2 fragment"
FT FT      1758..1787
FT FT      /*tag= al
FT FT      /note= "pref. V2 fragment"
FT FT      488..504
FT FT      /*tag= am
FT FT      /label= oligonucleotide_693
FT FT      /note= "used in NANBV cloning"
FT FT      complement (549..565)
FT FT      /*tag= an
FT FT      /label= oligonucleotide_694
FT FT      /note= "used in NANBV cloning"
FT FT      complement (581..701)
FT FT      /*tag= ao
FT FT      /label= oligonucleotide_691
FT FT      /note= "used in NANBV cloning"
FT FT      697..715
FT FT      /*tag= ap
FT FT      /label= oligonucleotide_14
FT FT      /note= "used in NANBV cloning"
FT FT      702..718
FT FT      /*tag= aq
FT FT      /label= oligonucleotide_15
FT FT      /note= "used in NANBV cloning"
FT FT      complement (853..870)
FT FT      /*tag= ar
FT FT      /label= oligonucleotide_18
FT FT      /note= "used in NANBV cloning"
FT FT      WO9203458-A.
FT PD      05-MAR-1992.
FT PF      23-AUG-1991; U06037.
FT PR      25-AUG-1990; US-573643.
FT PR      21-NOV-1990; US-616369.
FT PA      (NYBL-) NEW YORK BLOO DCENT.
FT PA      (PHAA-) PHARMACIA GENETIC ENG INC.
FT PI      Zebedee S, Inchauspe G, Nasofe MS, Prince AM;
FT DR      WPI; 92-096821/12..
FT DR      P-PSDB; R22154.
FT PT      Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis
FT PT      virus - Obtd. Hutch C59 subgroup encoding polypeptide(s), useful
FT PT      as vaccines, and immuno reactive Abs for diagnosis of virus
FT PS      Disclosure; Page 159-173; 225pp: English.
FT CC      One Hutch strain (HCV-H) of NANBV, designated the Hutch c59 isolate
FT CC      (HCV-Hc59) was propagated through passage in animals and the
FT CC      entire viral genome was cloned and sequenced.
FT CC      The sequence in Q22838 (tag u) comprises two bases, indicated in
FT CC      the features, which differ from the sequence represented here.
FT CC      Two more oligonucleotides used in NANBV cloning are shown in
FT CC      Q22838, and one in Q22859.
FT CC      The encoded proteins and peptides (see features) and antibodies
FT CC      against them are useful for the prepn. of vaccines and inoculums
FT CC      against NANBV and in immunological assays for detection of viral
FT CC      infection. The nucleic acid may be used to detect the presence of
FT CC      NANBV DNA.
FT CC      Nucleotide sequences used in the prodn. of polynucleotides are
FT CC      selected from the V, VI, V2 and V3 variable region. The regions
FT CC      indicated in the features encode peptides contg. the greatest amt. of
FT CC      diversity when compared to known HCV isolates. The polynucleotides
FT CC      may be used as primers, probes, or a nucleic acids.
FT SQ      Sequence 9416 BP; 1879 A; 2849 C; 2683 G; 2005 T;

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Query Match 100.0%; Score 20; DB 1; Length 9416;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggggagagccatagtgtc 20
|||||
Db 129 CCGGGAGAGCCATAGTGTC 148

RESULT 15
Q24467
ID Q24467 standard; DNA; 1880 BP.
AC Q24467;
DT 09-NOV-1992 (first entry)
DE NANB hepatitis virus strain HC-J4 genome.
KW non-A, non-B hepatitis virus; NANBH; PCR; amplification
KW polymerase chain reaction; vaccine; antibody; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 342..1880
FT /*tag= a
FT /label= HC-J4
FT EP-485209-A.
FT PN 13-MAY-1992.
FT PD
FT PF 07-NOV-1991; 310297.
FT PR 08-NOV-1990; JP-304405.
FT PA (IMMO) IMMUNO JAPAN INC.
FT PI Nakamura T, Okamoto H;
FT DR WPI; 92-160959/20.
FT DR P-PSDB; R24087.
FT PT Recombinant cDNA of NANBH virus strain HC-J5 and corresp.
FT PT peptides - useful for diagnosis and in vaccines and immunological
FT PT pharmaceuticals
FT PS Disclosure; Page 11; 42pp: English.
FT CC This sequence is the genome of the non-A, non-B hepatitis virus
FT CC (NANBH) strain HC-J4. This sequence was derived by amplification
FT CC by polymerase chain reaction. The nucleotide sequences derived from
FT CC this amplification can be used to detect NANBH infection which could
FT CC not be detected by conventional methods. The detection kits allow
FT CC highly specific and sensitive detection at an early phase of
FT CC infection. The polypeptide product of this coding sequence can be used
FT CC for the manufacture of vaccines and immunological pharmaceuticals
FT CC and also to produce antibodies specific to NANBH.
FT SQ Sequence 1880 BP; 333 A; 593 C; 556 G; 398 T;

Query Match 100.0%; Score 20; DB 1; Length 1880;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggggagagccatagtgtc 20
|||||
Db 129 CCGGGAGAGCCATAGTGTC 148

Search completed: November 23, 1999, 13:58:53
Job time: 6680 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 30, 1999, 17:10:23 ; Search time 27.26 Seconds
(without alignments)
165.204 Million cell updates/sec

Title: US-09-031-087-4
Perfect score: 18
Sequence: 1 cactatggctctccgga 18

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_16:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	9444	1	TL3279
2	17	94.4	9185	1	Q05956
3	17	94.4	9185	1	Q05956
4	17	94.4	504	1	Q12239
5	17	94.4	2116	1	Q12242
6	17	94.4	202	1	Q14083
7	17	94.4	202	1	Q14085
8	17	94.4	202	1	Q14086
9	17	94.4	202	1	Q14084
10	17	94.4	1863	1	Q15363
11	17	94.4	1863	1	Q15362
12	17	94.4	9416	1	Q21829
13	17	94.4	9416	1	Q20268
14	17	94.4	9400	1	Q21744
15	17	94.4	9416	1	Q22871
16	17	94.4	1880	1	Q24467
17	17	94.4	1886	1	Q24468
18	17	94.4	1880	1	Q24466
19	17	94.4	2540	1	Q29628
20	17	94.4	2540	1	Q29627
21	17	94.4	1885	1	Q29629
22	17	94.4	2551	1	Q29630
23	17	94.4	2498	1	Q29631
24	17	94.4	252	1	Q31071
25	17	94.4	252	1	Q31072
26	17	94.4	252	1	Q31078
27	17	94.4	252	1	Q31079
28	17	94.4	252	1	Q31066
29	17	94.4	252	1	Q31067
30	17	94.4	252	1	Q31068
31	17	94.4	252	1	Q31069
32	17	94.4	252	1	Q31070
33	17	94.4	252	1	Q31080
34	17	94.4	252	1	Q31081
35	17	94.4	180	1	Q31082
36	17	94.4	180	1	Q31083
37	17	94.4	483	1	Q32444
38	17	94.4	483	1	Q32445
39	17	94.4	483	1	Q32446
40	17	94.4	483	1	Q32447
41	17	94.4	1554	1	Q32451
42	17	94.4	483	1	Q32452
43	17	94.4	7911	1	Q32436

C 44 17 94.4 256 1 Q32981 HCV E1 5' non-codi
C 45 17 94.4 398 1 T01513 Hepatitis C virus

ALIGNMENTS

RESULT 1
TL3279
ID TL3279 standard; cDNA; 9444 BP.
AC TL3279;
DT 20-SEP-1996 (first entry)
DE cDNA to genomic hepatitis C virus RNA
KW hepatitis C virus; antibody; detection; diagnosis; vaccine;
KW classify; subtype; ss.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT cds complement (34..9105)
FT /*tag= a
PN J08056672-A.
PD 05-MAR-1996.
PF 26-AUG-1994; 223933.
PR 26-AUG-1994; JP-223933.
PA (SAYA/) SAYAMA K.
DR WPI: 96-182301/19.
DR P-PSDB; R94462.
DR Hepatitis C virus genomic RNA, DNA and related proteins - useful for
PT detection, diagnosis and identification of hepatitis C virus
PT sub-type
PS Claim 2: Page 9-12: 25pp; Japanese.
CC The present sequence represents cDNA to a hepatitis C virus (HCV)
CC genomic RNA. The sequence encodes a polypeptide contg. a 303 amino
CC acid sequence (see R94462) which can be easily detected by antibodies
CC in an assay for the detection of HCV. The DNA and the protein are
CC useful for classifying the subtype of HCV. At least a part of the
CC protein may be used as a vaccine against HCV.
SQ Sequence 9444 BP; 2079 A; 2608 C; 2682 G; 2075 T;
Query Match 100.0%; Score 18; DB 1; Length 9444;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cactatggctctccgga 18
|||||
DB 9302 CACTATGGCTCTCCCGGA 9319
RESULT 2
Q05956/c
ID Q05956 standard; DNA; 9185 BP.
AC Q05956;
DT 23-JAN-1991 (first entry)
DE Sense strand of the compiled Hepatitis C virus cDNA sequence.
KW Hepatitis C virus (HCV); antiviral agent; ss.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT cds 320..9185
FT /*tag= a
FT misc_rna 1..1667
FT /*tag= b
FT /*note="epitope within this region is claimed"
FT 8978..9185
FT /*tag= c
FT /*note="encodes an epitope that is claimed"
PN EP-388232-A.
PD 19-SEP-1990.
PF 16-MAR-1980; 302866.
PR 17-MAR-1989; US-325338.
PR 20-APR-1989; US-341134.
PR 18-MAY-1989; US-355002.
PA (CHIR-) CHIRON CORP.
PI Houghton M, Choo QL, Kuo G.

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DR WPI: 90-284418/38.
DR P-PSDB: R08124.
PT Hepatitis C virus DNA - used for producing probes,
PT polypeptide(s), antibodies and anti-sense polynucleotide(s) for
PT diagnosis and therapy.
PS Disclosure: Fig 17: 83pp; English.
CC HCV cDNA libraries were constructed using pooled serum from a
CC chimpanzee with chronic HCV infection. A lambda gill library was
CC screened with probes derived from previously isolated clones. The
CC ORF is derived from the overlapping clones b114a, ag30a, CA205a,
CC CA290a, CA216a, p14a, CA167b, CA156e, CA84a, CA59a, K9-1, 26j, 131,
CC 12f, 14i, 11b, 7f, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c,
CC 14c, 8f, 33f, 33g, 39c, 35f, 19q, 26g 15e, b5a and 16jh. These
CC clones extend the sequence of the HCV genome reported in EP-318216.
CC The upstream region from nucleotides -319 to +1348 (-1-1667 in this
CC file) is covered by clones b114a, 18g, ag30a, CA205a, CA290a,
CC CA216a, p14a, CA167b, CA156e, CA84a and CA59a; nucleotides
CC 8659-8866 (=8978-9185 in this file) are covered by clones b5a and
CC 16jh.
CC See also Q05955.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;

Query Match 94.4%; Score 17; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
| | | | | | | | | | | | | | | | | |
Db 123 CACTATGGCTCTCCCGG 107

RESULT 3
Q10566/c
ID Q10566 standard; DNA; 9185 BP.
AC Q10566;
DT 29-APR-1991 (first entry)
DE Hepatitis C virus strain 1 DNA.
KW Hepatitis C virus; HCV-1; non-A, non-B hepatitis; HCV antigen;
KW viral infections; ss.
OS Hepatitis C virus.
PN EP-414475-A.
PD 27-FEB-1991.
PF 21-AUG-1990; 309120.
PR 25-AUG-1989; US-398667.
PA (CHIR-) CHIRON CORP.
PI Weiner AJ, Steimer KS;
DR WPI: 91-059670/09.
PT Cell lines infected with hepatitis C virus - are used as source
PT of antigens for detection of HCV antibodies, for vaccines, and
PT for screening anti-viral agents
PS Disclosure: fig 1; 24pp; English.
CC This is a hepatitis C virus (HCV) composite cDNA sequence, deduced
CC using overlapping clones. a compsn. contg. the antigenic protein
CC encoded by this sequence is useful for detecting anti-HCV anti-
CC bodies (Abs) and for screening an agent which inhibits HCV replic-
CC ation. A cell line infected with this virus can be used as a
CC source of antigens. The antigen is useful for preparing vaccines
CC for treating viral infections. See also Q10567.
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T;

Query Match 94.4%; Score 17; DB 1; Length 9185;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
| | | | | | | | | | | | | | | | | |
Db 123 CACTATGGCTCTCCCGG 107

RESULT 4
Q12239/c
ID Q12239 standard; DNA; 504 BP.
AC Q12239;
DT 08-SEP-1991 (first entry)
DE Clone 164/137 encoding PT-NANBH virus antigenic portion.
DE post-transfusal non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT CDS 308..504
FT /tag= a
FT /product= start of PT-NANBH polypeptide
PN GB2239245-A.
PD 26-JUN-1991.
PF 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL ) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI: 91-187584/26.
DR P-PSDB: R12397.
PT Post-transfusal non-A non-B hepatitis poly:peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 71-72; 108pp; English.
CC This sequence probably encodes viral structural proteins of the
CC PT-NANBH viral genome having antigenic properties. It was
CC isolated from serum of humans infected by the virus.
CC See also Q12236-8 and Q12240-Q12242.
SQ Sequence 504 BP; 106 A; 147 C; 153 G; 98 T;

Query Match 94.4%; Score 17; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
| | | | | | | | | | | | | | | | | |
Db 111 CACTATGGCTCTCCCGG 95

RESULT 5
Q12242/c
ID Q12242 standard; DNA; 2116 BP.
AC Q12242;
DT 17-SEP-1991 (first entry)
DE Encodes PT-NANBH viral structural and non-structural proteins.
DE post-transfusal non-A, non-B hepatitis; virus; vaccine; ss.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT CDS 308..2116
FT /tag= a
FT GB2239245-A.
PD 26-JUN-1991.
PF 17-DEC-1990; 027250.
PR 18-DEC-1989; GB-028562.
PR 27-FEB-1990; GB-004414.
PR 03-MAR-1990; GB-004814.
PR 17-DEC-1990; GB-027250.
PA (WELL ) WELLCOME FOUNDATION LTD.
PI Highfield PE, Rodgers BC, Tedder RS, Barbara JAJ;
DR WPI: 91-187584/26.
DR P-PSDB: R12800.
PT Post-transfusal non-A non-B hepatitis poly:peptide(s) - and
PT also DNA and antibodies used in diagnostic assays and in vaccines
PS Claim 10; Page 83-87; 108pp; English.
CC This sequence is thought to encode viral structural and non-
CC structural proteins of the PT-NANBH viral genome which are antigenic.
CC It was isolated from human serum infectious for the virus.
CC See also Q12236-41.
SQ Sequence 2116 BP; 392 A; 650 C; 624 G; 450 T;

Query Match 94.4%; Score 17; DB 1; Length 2116;

```

Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
|||||
Db 111 CACTATGGCTCTCCGG 95

RESULT 6

Q14083/C
ID Q14083 standard; DNA; 202 BP.
AC Q14083;
DT 03-JAN-1992 (first entry)
DE HCV-T (1-202).
KW Epitope; PCR; diagnosis; ss.
OS Hepatitis C virus.
PN WO9114779-A.
PD 03-OCT-1991.
PF 28-MAR-1991; J00405.
PR 28-MAR-1990; JP-080185.
PR 13-JUN-1990; JP-154230.
PR 14-JUN-1990; JP-153979.
PR 09-NOV-1990; JP-305795.
PA (MITK) MITSUI TOATSU CHEM INC.
PI Takada T, Enomoto N, Date T, Nakao T;
DR WPI; 91-310579/42.
PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
PT of hepatitis C virus infection via polymerase chain reaction
PS Disclosure; Fig 1(1); 79pp; Japanese.
CC The nucleotide sequences represented in Q14076-86 and Q14767-71
CC encode epitopes from structural, non-structural and 5' untranslated
CC domains of hepatitis C virus. The sequences are used for accurate
CC and simple diagnosis and typing of HCV infection, using PCR
CC amplification techniques.
SQ Sequence 202 BP; 39 A; 61 C; 61 G; 41 T;

Query Match 94.4%; Score 17; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
|||||
Db 102 CACTATGGCTCTCCGG 86

RESULT 7

Q14085/C
ID Q14085 standard; DNA; 202 BP.
AC Q14085;
DT 03-JAN-1992 (first entry)
DE HCV-KU (1-202).
KW Epitope; PCR; diagnosis; ss.
OS Hepatitis C virus.
PN WO9114779-A.
PD 03-OCT-1991.
PF 28-MAR-1991; J00405.
PR 28-MAR-1990; JP-080185.
PR 13-JUN-1990; JP-154230.
PR 14-JUN-1990; JP-153979.
PR 09-NOV-1990; JP-305795.
PA (MITK) MITSUI TOATSU CHEM INC.
PI Takada T, Enomoto N, Date T, Nakao T;
DR WPI; 91-310579/42.
PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
PT of hepatitis C virus infection via polymerase chain reaction
PS Disclosure; Fig 1(1); 79pp; Japanese.
CC The nucleotide sequences represented in Q14076-86 and Q14767-71
CC encode epitopes from structural, non-structural and 5' untranslated
CC domains of hepatitis C virus. The sequences are used for accurate
CC and simple diagnosis and typing of HCV infection, using PCR
CC amplification techniques.
SQ Sequence 202 BP; 40 A; 61 C; 58 G; 43 T;

Query Match 94.4%; Score 17; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
|||||
Db 102 CACTATGGCTCTCCGG 86

RESULT 8

Q14086/C
ID Q14086 standard; DNA; 202 BP.
AC Q14086;
DT 03-JAN-1992 (first entry)
DE HCV-N (1-200).
KW Epitope; PCR; diagnosis; ss.
OS Hepatitis C virus.
PN WO9114779-A.
PD 03-OCT-1991.
PF 28-MAR-1991; J00405.
PR 28-MAR-1990; JP-080185.
PR 13-JUN-1990; JP-154230.
PR 14-JUN-1990; JP-153979.
PR 09-NOV-1990; JP-305795.
PA (MITK) MITSUI TOATSU CHEM INC.
PI Takada T, Enomoto N, Date T, Nakao T;
DR WPI; 91-310579/42.
PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
PT of hepatitis C virus infection via polymerase chain reaction
PS Disclosure; Fig 1(1); 79pp; Japanese.
CC The nucleotide sequences represented in Q14076-86 and Q14767-71
CC encode epitopes from structural, non-structural and 5' untranslated
CC domains of hepatitis C virus. The sequences are used for accurate
CC and simple diagnosis and typing of HCV infection, using PCR
CC amplification techniques.
SQ Sequence 202 BP; 42 A; 60 C; 56 G; 44 T;

Query Match 94.4%; Score 17; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
|||||
Db 102 CACTATGGCTCTCCGG 86

RESULT 9

Q14084/C
ID Q14084 standard; DNA; 202 BP.
AC Q14084;
DT 03-JAN-1992 (first entry)
DE HCV-I (1-202).
KW Epitope; PCR; diagnosis; ss.
OS Hepatitis C virus.
PN WO9114779-A.
PD 03-OCT-1991.
PF 28-MAR-1991; J00405.
PR 28-MAR-1990; JP-080185.
PR 13-JUN-1990; JP-154230.
PR 14-JUN-1990; JP-153979.
PR 09-NOV-1990; JP-305795.
PA (MITK) MITSUI TOATSU CHEM INC.
PI Takada T, Enomoto N, Date T, Nakao T;
DR WPI; 91-310579/42.
PT New nucleotide sequences encoding HCV epitope(s) - for diagnosis
PT of hepatitis C virus infection via polymerase chain reaction
PS Disclosure; Fig 1(1); 79pp; Japanese.
CC The nucleotide sequences represented in Q14076-86 and Q14767-71
CC encode epitopes from structural, non-structural and 5' untranslated
CC domains of hepatitis C virus. The sequences are used for accurate

CC and simple diagnosis and typing of HCV infection, using PCR
CC amplification techniques.
SQ Sequence 202 BP; 41 A; 60 C; 60 G; 41 T;

Query Match 94.4%; Score 17; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

Qy 1 cactatggctctcccg 17
|||||
Db 102 CACTATGGCTCTCCCG 86

RESULT 10

Q15363/C
ID Q15363 standard; DNA; 1863 BP.
AC Q15363.
DT 17-MAR-1992 (first entry)
DE Fragment of NANB hepatitis virus strain HC-J4.
KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
KW polymerase chain reaction; ss.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT 5'utr 1..324
FT cds /*tag= a
FT 325..1863
FT /*tag= b

PN EP-461863-A.

PD 18-DEC-1991.

PF 11-JUN-1991; 305270.

PR 12-JUN-1990; JP-153402.

PA (IMMU-) IMMUNO JAPAN INC.

PI Okamoto H, Ogikubo Y;

DR WPI; 91-370834/51.

PT Oligo-nucleotide primers - derived from and used to detect and

PT diagnose non-A, non-B hepatitis virus

PS claim 1; Page 7; 23pp; English.

CC NANB hepatitis virus strain HC-J4 was isolated from a plasma sample

CC of a chimpanzee challenged with NANB hepatitis for infectivity but

CC which tested negative for HCV antibody by Ortho HCV Ab ELISA test.

CC RNA was isolated from the sample and reverse transcribed into cDNA.

CC The 513 amino acids encoded by the CDS were determined but are not

CC given in the specification (and hence are not included in A-GeneSeq).

CC A study of the deduced sequence suggested that the CDS encodes NANBH

CC virus core proteins. Primers for detecting NANB hepatitis virus were

CC designed based on the HC-J4 sequence.

CC Sequence 1863 BP; 333 A; 586 C; 547 G; 397 T;

SQ

Query Match 94.4%; Score 17; DB 1; Length 1863;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctcccg 17
|||||
Db 128 CACTATGGCTCTCCCG 112

RESULT 11

Q15362/C
ID Q15362 standard; cDNA; 1863 BP.
AC Q15362;
DT 17-MAR-1992 (first entry)
DE Fragment of NANB hepatitis virus strain HC-J1.
KW Post-transfusion; non-A, non-B hepatitis; HCV; detection primer; PCR;
KW polymerase chain reaction; ss.
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT 5'utr 1..324
FT /*tag= a
FT 325..1863
FT /*tag= b

PN EP-461863-A.

PD 08-JAN-1992.

PF 28-DEC-1990; 314371.

PR 25-JUN-1990; JP-167466.

PN EP-461863-A.
PD 18-DEC-1991.
PF 11-JUN-1991; 305270.
PR 12-JUN-1990; JP-153402.
PA (IMMU-) IMMUNO JAPAN INC.
PI Okamoto H, Ogikubo Y;
DR WPI; 91-370834/51.
PT Oligo-nucleotide primers - derived from and used to detect and
PT diagnose non-A, non-B hepatitis virus
PS claim 1; Page 7; 23pp; English.
CC NANB hepatitis virus strain HC-J1 was isolated from a plasma sample
CC of a Japanese blood donor who tested positive for HCV antibody. RNA
CC was isolated from the sample and reverse transcribed into cDNA. The
CC 513 amino acids encoded by the CDS were determined but are not given
CC in the specification (and hence are not included in A-GeneSeq). A
CC study of the deduced sequence suggested that the CDS encodes NANBH
CC virus core proteins. Primers for detecting NANB hepatitis virus were
CC designed based on the HC-J1 sequence.
CC Sequence 1863 BP; 347 A; 581 C; 533 G; 402 T;
SQ

Query Match 94.4%; Score 17; DB 1; Length 1863;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctcccg 17
|||||
Db 128 CACTATGGCTCTCCCG 112

RESULT 12

Q21829/C
ID Q21829 standard; cDNA; 9416 BP.
AC Q21829;
DT 01-MAY-1992 (first entry)
DE Non-A, non-B viral genome.
KW NANBV; vaccine; immunodiagnosis; antigen; antibody; ds.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT cds 333..677
FT /*tag= a
FT /*product= C
FT /*note= "core protein"
FT cds 678..905
FT /*tag= b
FT /*product= M
FT /*note= "matrix protein"
FT cds 906..1499
FT /*tag= C
FT /*product= E
FT /*note= "envelope protein"
FT cds 1500..2519
FT /*tag= d
FT /*product= NS1
FT cds 2520..3350
FT /*tag= e
FT /*product= NS2
FT cds 3351..5177
FT /*tag= f
FT /*product= NS3
FT cds 5178..5918
FT /*tag= g
FT /*product= NS4a
FT cds 5919..6371
FT /*tag= h
FT /*product= NS4b
FT cds 6372..9365
FT /*tag= i
FT /*product= NS5

PN EP-464287-A.

PD 08-JAN-1992.

PF 28-DEC-1990; 314371.

PR 25-JUN-1990; JP-167466.

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PR 31-AUG-1990; JP-230921.
PR 09-NOV-1990; JP-305605.
PA (OSAU ) Osaka University.
PI Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
DR WPI: 92-009617/02.
DR P-PSDB; R20091.
PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
PT diagnostics and screening agents for NANBV, and to remove NANBV from
PT blood.
PS Claim 1; Fig 2; 89pp; English.
CC The sequence was obtd. from several overlapping "BK" cDNA clones
CC obtd. by "gene walking" using a cDNA clone isolated from a library
CC prep'd. from NANBV RNA. The DNA and fragments of it can be used
CC for the detection of the presence of NANBV by hybridisation or PCR.
CC Antigenic polypeptides encoded by the sequence can be used as
CC immunoassay reagents, for screening donated blood, and as immuno-
CC gens for vaccine prodn. Antibodies raised to the peptides can be
CC used in immunoassays to detect or quantify NANBV antigens in liver
CC tissue and blood. Preferred polypeptides are encoded by the
CC following nucleotides: 333-422, 677, or -6371; 474-563; 678-905;
CC 906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
CC 2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5919-
CC 6371; and 6372-9372. The sequence is also disclosed in EP-463848
CC in which a virus particle contg. antigens encoded by the sequence
CC is claimed, as well as expression vectors contg. the sequence.
CC See Q20268 for details of this specification.
CC Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;
SQ

Query Match 94.4%; Score 17; DB 1; Length 9416;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cactatggctctccgg 17
|||||
DB 136 CACTATGGCTCTCCGG 120

RESULT 13
Q20268/c
ID Q20268 standard; cDNA; 9416 BP.
AC Q20268;
DT 01-MAY-1992 (first entry)
DE Non-A, non-B viral genome.
KW NANBV; vaccine; immunodiagnosis; antigen; antibody; ds.
OS Non-A, non-B hepatitis virus.
FH Key Location/Qualifiers
FT 333..677
FT /*tag= a
FT /*product= C
FT /*note= "core protein"
FT 678..905
FT /*tag= b
FT /*product= M
FT /*note= "matrix protein"
FT 906..1499
FT /*tag= c
FT /*product= E
FT /*note= "envelope protein"
FT 1500..2519
FT /*tag= d
FT /*product= NS1
FT 2520..3350
FT /*tag= e
FT /*product= NS2
FT 3351..5177
FT /*tag= f
FT /*product= NS3
FT 5178..5918
FT /*tag= g
FT /*product= NS4a
FT 5919..6371
FT /*tag= h

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FT cds
FT /product= NS4b
FT 6372..9365
FT /*tag= i
FT /product= NS5
PD EP-463848-A.
PD 02-JAN-1991.
PD 25-JUN-1991; 305717.
PD 25-JUN-1990; JP-167466.
PR 31-AUG-1990; JP-230921.
PR 09-NOV-1990; JP-305605.
PR 28-DEC-1990; US-635451.
PR 08-MAY-1991; JP-132090.
PR 14-MAY-1991; JP-138493.
PA (OSAU ) Osaka University.
PI Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
DR WPI: 92-009412/02.
DR P-PSDB; R20111.
PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
PT diagnostics and screening agents for NANBV, and to remove NANBV from
PT blood.
PS Disclosure; Fig 2; 89pp; English.
CC The sequence was obtd. from several overlapping "BK" cDNA clones
CC obtd. by "gene walking" using a cDNA clone isolated from a library
CC prep'd. from NANBV RNA. The DNA and fragments of it can be used
CC for the detection of the presence of NANBV by hybridisation or PCR.
CC Antigenic polypeptides encoded by the sequence can be used as
CC immunoassay reagents, for screening donated blood, and as immuno-
CC gens for vaccine prodn. Antibodies raised to the peptides can be
CC used in immunoassays to detect or quantify NANBV antigens in liver
CC tissue and blood. Preferred polypeptides are encoded by the
CC following nucleotides: 333-422, -677, or -6371; 474-563; 678-905;
CC 906-953 or -1499; 1020-1046 or -1121; 1194-1232; 1209-1322; 1500-
CC 2519; 2520-3350; 3351-5177; 4485-4574; 5178-5918; 5544-5633; 5919-
CC 6371; and 6372-9372. The sequence is also disclosed in EP-464287
CC in which it is claimed. See Q21829 for details of this specifii-
CC cation.
CC Sequence 9416 BP; 1905 A; 2825 C; 2679 G; 2007 T;
SQ

Query Match 94.4%; Score 17; DB 1; Length 9416;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cactatggctctccgg 17
|||||
DB 136 CACTATGGCTCTCCGG 120

RESULT 14
Q21744/c
ID Q21744 standard; DNA; 9400 BP.
AC Q21744;
DT 22-JUN-1992 (first entry)
DE Compiled HCV cDNA.
KW HCV; serum; gtl1; oligomer; target; ds.
OS Hepatitis C virus 1.
FH Key Location/Qualifiers
FT 341..9373
FT /*tag= a
FT /*label= polyprotein
FT 357..386
FT /*tag= b
FT /*label= target_region
FT /*note= "see CC"
FT 390..419
FT /*tag= c
FT /*label= target_region
FT /*note= "see CC"
FT 423..452
FT /*tag= d
FT /*label= target_region
FT /*note= "see CC"
FT 456..485
FT /*label= target_region

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FT /*tag= e
FT /label= target_region
FT /note= "see CC"
FT 489. .518
FT /*tag= f
FT /label= target_region
FT /note= "see CC"
FT 552. .581
FT /*tag= g
FT /label= target_region
FT /note= "see CC"
FT 583. .612
FT /*tag= h
FT /label= target_region
FT /note= "see CC"
FT 616. .645
FT /*tag= i
FT /label= target_region
FT /note= "see CC"
FT 673. .702
FT /*tag= j
FT /label= target_region
FT /note= "see CC"
FT 706. .735
FT /*tag= k
FT /label= target_region
FT /note= "see CC"
FT 739. .768
FT /*tag= l
FT /label= target_region
FT /note= "see CC"
FT 798. .827
FT /*tag= m
FT /label= target_region
FT /note= "see CC"

FT WO9202642-A.

PN 20-FEB-1992.

PD 12-AUG-1991; U05728.

PF 10-AUG-1990; US-566209.

PR (CHIR-) CHIRON CORP.

PI Houghton M, Choo QL, Kuo G, Weiner AJ, Urdea MS, Irvine BD;

PI Kolberg JA;

DR P-PSDB: R21519.

PT Reagents for isolating, amplifying and detecting HCV

PT polynucleotide(s) - used to monitor spread of blood-borne non-A,

PT non-B hepatitis virus infection and screen blood samples for

PT virus

PS Disclosure: Fig 1: 67pp: English.

CC The sequence is a composite of HCV cDNA from HCV1, a prototypic

CC HCV. The sequence is based upon sequence information derived from

CC a no. of HCV cDNA clones, which were isolated from a no. of HCV

CC cDNA libraries, including the "c" library present in lambda gt11

CC (ATCC No.40394), and from human serum. The HCV cDNA clones

CC were isolated by methods described in WO9014436.

CC The clones from which the sequence was derived are 5' clones32,

CC b114a, 18g, ag30a, CA205a, CA290g, CA216a, p114a, CA167b, CA156e,

CC CA84a, CA59a, K9-1 (also called K9-1), 26j, 13i, 12f, 14i, 11b, 7f,

CC 7e, 8i, 33c, 40b, 37b, 35, 36, 8i, 32, 33b, 25c, 14c, 8f, 33f, 33g,

CC 39c, 35f, 19g, 26g, 15e, b5a, 16jh, 6k and p131jh.

CC The target regions indicated in the features are listed in claim 1,

CC page 49. Oligomers are provided which are complementary to these

CC target regions and used in the detection of an HCV sequence in an

CC analyte.

SQ Sequence 9400 BP: 1885 A: 2860 C: 2671 G: 1984 T;

Query Match 94.4% Score 17: DB 1: Length 9400;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Qy 1 cactatggctctcccg 17

|||||

Db 145 CACTATGGCTCTCCCG 129

RESULT 15

Q22871/c

ID Q22871 standard; DNA; 9416 BP.

AC Q22871;

DT 07-JUL-1992 (first entry)

DE NANBV Hutch c59 isolate genome.

KW Hepatitis C virus; non-A non-B virus; HCV-Hc59; primers;

KW Probes; vaccine; ss.

OS NANBV Hutch c59 isolate.

FH Key Location/Qualifiers

FT 342. .9377

FT /*tag= a

FT /label= viral_genome

FT 1. .12

FT /*tag= b

FT /note= "not confirmed as HCV-Hc59 sequence"

FT 9397. .9416

FT /*tag= c

FT /note= "not confirmed as HCV-Hc59 sequence"

FT 7. .12

FT /*tag= d

FT /rpt_type= 1

FT 42. .47

FT /*tag= e

FT /rpt_type= 1

FT 23. .28

FT /*tag= f

FT /rpt_type= 2

FT 38. .43

FT /*tag= g

FT /rpt_type= 2

FT 9209. .9214

FT /*tag= h

FT /rpt_type= 2

FT 9391. .9396

FT /*tag= i

FT /rpt_type= 2

FT 128. .135

FT /*tag= j

FT /rpt_type= 3

FT 315. .322

FT /*tag= k

FT /rpt_type= 3

FT 315. .322

FT /*tag= l

FT /rpt_type= 3

FT 9231. .9237

FT /*tag= m

FT /rpt_type= 4

FT 9245. .9251

FT /*tag= n

FT /rpt_type= 4

FT 9256. .9262

FT /*tag= o

FT /rpt_type= 4

FT 9248. .9253

FT /*tag= p

FT /rpt_type= 5

FT 9221. .9226

FT /*tag= q

FT /rpt_type= 5

FT 9227. .9232

FT /*tag= r

FT /rpt_type= 5

FT 351. .353

FT /*tag= s

FT /label= AAT

FT /note= "or ATT according to Seq No 1 (Q22838), see CC"

FT 1302. .1304

FT /*tag= t

FT misc_difference

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FT /label= AAT
FT /note= "or GAT according to Seq No 1 (Q22838). see CC"
FT 342. .1319
FT /tag= u
FT /product= NANBV_structural_proteins
FT /note= "Seq No 1 (Q22838)"
FT 342. .701
FT /tag= v
FT /label= capsid
FT 702. .1319
FT /tag= w
FT /label= envelope_protein
FT 1. .60
FT /tag= x
FT /label=
FT /note= "pref. capsid antigen"
FT 61. .120
FT /tag= y
FT /note= "pref. capsid antigen"
FT 4. .120
FT /tag= z
FT /note= "pref. capsid antigen"
FT 1. .222
FT /tag= aa
FT /note= "pref. capsid antigen"
FT 205. .360
FT /tag= ab
FT /note= "pref. capsid antigen"
FT 361. .528
FT /tag= ac
FT /note= "pref. envelope antigen"
FT 361. .978
FT /tag= ad
FT /note= "pref. envelope antigen"
FT 1497. .1574
FT /tag= ae
FT /label= V_variable_region
FT 1077. .1166
FT /tag= af
FT /label= V1_variable_region
FT 1707. .1787
FT /tag= ag
FT /label= V2_variable_region
FT 7407. .7478
FT /tag= ah
FT /label= V3_variable_region
FT 1512. .1553
FT /tag= ai
FT /note= "pref. V fragment"
FT 1077. .1109
FT /tag= aj
FT /note= "pref. V1 fragment"
FT 1722. .1739
FT /tag= ak
FT /note= "pref. V2 fragment"
FT 1758. .1787
FT /tag= al
FT /note= "pref. V2 fragment"
FT 488. .504
FT /tag= am
FT /label= oligonucleotide_693
FT /note= "used in NANBV cloning"
FT complement (549. .565)
FT /tag= an
FT /label= oligonucleotide_694
FT /note= "used in NANBV cloning"
FT complement (581. .701)
FT /tag= ao
FT /label= oligonucleotide_691
FT /note= "used in NANBV cloning"
FT 697. .715
FT /tag= ap
FT /label= oligonucleotide_14
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FT misc_rna
FT 702. .718
FT /tag= aq
FT /label= oligonucleotide_15
FT /note= "used in NANBV cloning"
FT complement (853. .870)
FT /tag= ar
FT /label= oligonucleotide_18
FT /note= "used in NANBV cloning"
FT
FT WO9203458-A.
FT 05-MAR-1992.
FT 23-AUG-1991: U06037.
FT 25-AUG-1990: US-573643.
FT 21-NOV-1990: US-616369.
FT (NYBL-) NEW YORK BLOO DCENT.
FT (PHAA ) PHARMACIA GENETIC ENG INC.
FT Zebedee S, Inchauspe G, Nasofe MS, Prince AM;
FT WPI: 92-096821/12.
FT P-PSDB: R22154.
FT Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis
FT virus - obtd. Hutch C59 subgroup encoding polypeptide(s), useful
FT as vaccines, and immuno reactive Abs for diagnosis of virus
FT Disclosure; Page 159-173; 225pp; English.
FT One Hutch strain (HCV-H) of NANBV, designated the Hutch C59 isolate
FT (HCV-Hc59) was propagated through passage in animals and the
FT entire viral genome was cloned and sequenced.
FT The sequence in Q22838 (tag u) comprises two bases, indicated in
FT the features, which differ from the sequence represented here.
FT Two more oligonucleotides used in NANBV cloning are shown in
FT CC Q22838, and one in Q22859.
FT CC The encoded proteins and peptides (see features) and antibodies
FT against them are useful for the prepn. of vaccines and inoculums
FT against NANBV and in immunological assays for detection of viral
FT infection. The nucleic acid may be used to detect the presence of
FT CC NANBV DNA.
FT CC Nucleotide sequences used in the prodn. of polynucleotides are
FT selected from the V, V1, V2 and V3 variable region. The regions
FT indicated in the features encode peptides contg. the greatest amt. of
FT diversity when compared to known HCV isolates. The polynucleotides
FT may be used as primers, probes, or a nucleic acids.
FT Sequence 9416 BP; 1879 A; 2849 C; 2683 G; 2005 T;
FT SQ
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Query Match 94.4%; Score 17; DB 1; Length 9416;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cactatggctctccgg 17
Db 145 CACTATGGCTCTCCCG 129

Search completed: November 30, 1999, 18:36:11
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